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NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	3	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	4	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	5	APR 28	IMSRESEARCH reloaded with enhancements
NEWS	6	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	7	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	8	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	9	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	10	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	11	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	12	JUN 25	CA/CAPLUS and USPAT databases updated with IPC reclassification data
NEWS	13	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	14	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations
NEWS	15	JUN 30	STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in
NEWS	16	JUN 30	STN AnaVist enhanced with database content from EPFULL
NEWS	17	JUL 28	CA/CAPLUS patent coverage enhanced
NEWS	18	JUL 28	EPFULL enhanced with additional legal status information from the epoline Register
NEWS	19	JUL 28	IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS	20	JUL 28	STN Viewer performance improved
NEWS	21	AUG 01	INPADOCDB and INPAFAMDB coverage enhanced
NEWS	22	AUG 13	CA/CAPLUS enhanced with printed Chemical Abstracts page images from 1967-1998
NEWS	23	AUG 15	CAOLD to be discontinued on December 31, 2008
NEWS	24	AUG 15	CAPLUS currency for Korean patents enhanced
NEWS	25	AUG 25	CA/CAPLUS, CASREACT, and IFI and USPAT databases enhanced for more flexible patent number searching
NEWS	26	AUG 27	CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information
NEWS	27	SEP 18	Support for STN Express, Versions 6.01 and earlier, to be discontinued
NEWS	28	SEP 25	CA/CAPLUS current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances

NEWS 29 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and  
and Korean patents enhanced  
NEWS 30 SEP 29 IFICLS enhanced with new super search field  
NEWS 31 SEP 29 EMBASE and EMBAL enhanced with new search and  
display fields  
NEWS 32 SEP 30 CAS patent coverage enhanced to include exemplified  
prophetic substances identified in new Japanese-  
language patents

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,  
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability  
NEWS LOGIN Welcome Banner and News Items  
NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that  
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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 04:02:48 ON 01 OCT 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED  
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.21	0.21

FULL ESTIMATED COST

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,  
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,  
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,  
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 04:03:14 ON 01 OCT 2008

69 FILES IN THE FILE LIST IN STINDEX

Enter SET DETAIL ON to see search term postings or to view  
search error messages that display as 0\* with SET DETAIL OFF.

=> s biofilm and remov?(p)biofilm and protease and esterase and amylase and solut?  
and alkaline and wash?

0\* FILE ADISNEWS  
0\* FILE ANTE  
0\* FILE AQUALINE  
0\* FILE BIOENG  
0\* FILE BIOTECHABS  
0\* FILE BIOTECHDS  
0\* FILE BIOTECHNO  
0\* FILE CEABA-VTB  
0\* FILE CIN  
0\* FILE ESBIODASE

30 FILES SEARCHED...

0\* FILE FOMAD  
0\* FILE FOREGE  
0\* FILE FROSTI  
0\* FILE FSTA

```

1 FILE GENBANK
1 FILE IFIPAT
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
60 FILES SEARCHED...
11 FILE USPATFULL
4 FILE USPAT2
0* FILE WATER

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4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STINDEX

L1 QUE BIOFILM AND REMOV?(P) BIOFILM AND PROTEASE AND ESTERASE AND AMYLASE AND SOLUT? AND ALKALINE AND WASH?

=> file genbank ifipat uspatfull uspat2  
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
2.60	2.81

FULL ESTIMATED COST

FILE 'GENBANK' ENTERED AT 04:05:30 ON 01 OCT 2008

FILE 'IFIPAT' ENTERED AT 04:05:30 ON 01 OCT 2008  
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'USPATFULL' ENTERED AT 04:05:30 ON 01 OCT 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 04:05:30 ON 01 OCT 2008  
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l1  
L2 17 L1

=> dup rem l2  
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.  
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE  
PROCESSING COMPLETED FOR L2  
L3 13 DUP REM L2 (4 DUPLICATES REMOVED)

=> d l3 1-13

```

L3 ANSWER 1 OF 13 USPATFULL on STN
AN 2008:29739 USPATFULL
TI Removable antimicrobial coating compositions and methods of use
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES
Hoffmann, Christian, Newark, DE, UNITED STATES
Lenges, Christian Peter, Wilmington, DE, UNITED STATES
Stieglitz, Barry, Wynnewood, PA, UNITED STATES
Leger, Lynn, Mississauga, CANADA
VanGorp, Judith Johanna, Wilmington, DE, UNITED STATES
Malone, Shaun F., Ajax, CANADA
PI US 20080026026 A1 20080131
AI US 2007-710290 A1 20070223 (11)
FRAI US 2006-776081P 20060223 (60)
US 2006-831983P 20060719 (60)
DT Utility
FS APPLICATION
LN.CNT 2260
INCL INCLM: 424/405.000

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INCLS: 422/028.000  
NCL NCLM: 424/405.000  
NCLS: 422/028.000  
IC IPCI A01N0025-00 [I,A]; A01P0001-00 [I,A]; A61L0002-00 [I,A]  
IPCR A01N0025-00 [I,C]; A01N0025-00 [I,A]; A01P0001-00 [I,C];  
A01P0001-00 [I,A]; A61L0002-00 [I,C]; A61L0002-00 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 13 USPATFULL on STN  
AN 2007:314900 USPATFULL  
TI Removable antimicrobial coating compositions and methods of use  
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES  
Hoffmann, Christian, Newark, DE, UNITED STATES  
Lenges, Christian Peter, Wilmington, DE, UNITED STATES  
Leger, Lynn, Mississauga, CANADA  
Malone, Shaun F., Ajax, CANADA  
Stieglitz, Barry, Wynnewood, PA, UNITED STATES  
Van Gorp, Judith Johanna, Wilmington, DE, UNITED STATES  
PI US 20070275101 A1 20071129  
AI US 2007-710325 A1 20070223 (11)  
PRAI US 2006-776081P 20060223 (60)  
US 2006-831983P 20060719 (60)

DT Utility  
FS APPLICATION  
LN.CNT 2259  
INCL INCLM: 424/719.000  
INCLS: 106/015.050; 514/642.000  
NCL NCLM: 424/719.000  
NCLS: 106/015.050; 514/642.000

IC IPCI A01N0033-12 [I,A]; A01N0033-00 [I,C\*]; A01P0001-00 [I,A];  
A01P0013-00 [I,A]; A01P0003-00 [I,A]  
IPCR A01N0033-00 [I,C]; A01N0033-12 [I,A]; A01P0001-00 [I,C];  
A01P0001-00 [I,A]; A01P0003-00 [I,C]; A01P0003-00 [I,A];  
A01P0013-00 [I,C]; A01P0013-00 [I,A]  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 13 IFIPAT COPYRIGHT 2008 IFI on STN  
AN 10840879 IFIPAT;IFIUDB;IFICDB  
TI Method of removing a biofilm; Washing  
simultaneously or consecutively in solution comprising an  
enzyme mixture containing at least one protease, at least one  
esterase, and an amylase in a detergent with an  
alkaline pH  
IN Marion Karine  
PA Unassigned Or Assigned To Individual (68000)  
PPA karine Marion thierry Sanchez (Probable)  
PI US 20050079594 A1 20050414  
AI US 2003-695823 20031030  
PRAI FR 2002-13963 20021031  
US 2002-422508P 20021031 (Provisional)  
FI US 20050079594 20050414  
DT Utility; Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
ED Entered STN: 19 Apr 2005  
Last Updated on STN: 23 Aug 2007  
CLMN 22

L3 ANSWER 4 OF 13 USPATFULL on STN  
AN 2005:208966 USPATFULL  
TI Protein variants having modified immunogenicity  
IN Roggen, Erwin Ludo, Lyngby, DENMARK

Ernst, Steffen, Broenshoej, DENMARK  
Svendsen, Allan, Hoersholm, DENMARK  
Friis, Esben Peter, Valby, DENMARK  
Osten, Claus Von Der, Lyngby, DENMARK  
PA Novozymes A/S, Bagsvaerd, DENMARK (non-U.S. corporation)  
PI US 20050181446 A1 20050818  
AI US 2001-957806 A1 20010921 (9)  
PRAI WO 2001-DK293 20010430  
DK 2000-707 20000428  
DK 2001-327 20010228  
US 2000-203345P 20000510 (60)  
US 2001-277817P 20010321 (60)

DT Utility  
FS APPLICATION  
LN.CNT 12950  
INCL INCLM: 435/007.100  
INCLS: 435/069.100; 435/320.100; 435/325.000; 702/019.000; 435/005.000  
NCL NCLM: 435/007.100  
NCLS: 435/005.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;  
506/014.000; 530/350.000; 702/019.000

IC [7]  
ICM C12Q001-70  
ICS G01N033-53; G06F019-00; G01N033-48; G01N033-50; C12P021-02;  
C12N005-06  
IPCI C12Q0001-70 [ICM,7]; G01N0033-53 [ICS,7]; G06F0019-00 [ICS,7];  
G01N0033-48 [ICS,7]; G01N0033-50 [ICS,7]; C12P0021-02 [ICS,7];  
C12N0005-06 [ICS,7]  
IPCR A21D0002-00 [I,C\*]; A21D0002-26 [I,A]; A21D0008-02 [I,C\*];  
A21D0008-04 [I,A]; C07K0001-00 [I,C\*]; C07K0001-04 [I,A];  
C07K0005-00 [I,C\*]; C07K0005-103 [I,A]; C07K0005-11 [I,A];  
C07K0005-113 [I,A]; C07K0016-40 [I,C\*]; C07K0016-40 [I,A];  
C11D0003-38 [I,C\*]; C11D0003-386 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 13 USPATFULL on STN  
AN 2005:104955 USPATFULL  
TI Multimolecular devices and drug delivery systems  
IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES  
PI US 20050089890 A1 20050428  
AI US 2004-872973 A1 20040621 (10)  
RLI Division of Ser. No. US 2001-907385, filed on 17 Jul 2001, GRANTED, Pat.  
No. US 6762025 Continuation of Ser. No. US 1998-81930, filed on 20 May  
1998, GRANTED, Pat. No. US 6287765

DT Utility  
FS APPLICATION  
LN.CNT 15620  
INCL INCLM: 435/006.000  
INCLS: 530/395.000  
NCL NCLM: 435/006.000  
NCLS: 530/395.000

IC [7]  
ICM C12Q001-68  
ICS C07K014-00  
IPCI C12Q0001-68 [ICM,7]; C07K0014-00 [ICS,7]  
IPCR C07H0021-00 [I,C\*]; C07H0021-00 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 6 OF 13 USPATFULL on STN DUPLICATE 1  
AN 2004:144188 USPATFULL  
TI METHODS FOR ELIMINATING THE FORMATION OF BIOFILM  
IN Xu, Feng, Davis, CA, UNITED STATES  
PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.

corporation)  
 PI US 20040109852 A1 20040610  
 US 6777223 B2 20040817  
 AI US 2001-885379 A1 20010619 (9)  
 RLI Continuation-in-part of Ser. No. US 2000-596795, filed on 19 Jun 2000,  
 ABANDONED  
 DT Utility  
 FS APPLICATION  
 LN.CNT 995  
 INCL INCLM: 424/094.600  
 INCLS: 424/094.200  
 NCL NCLM: 435/262.500; 424/094.600  
 NCLS: 210/632.000; 424/094.100; 424/094.200; 435/189.000; 435/190.000  
 IC [7]  
 ICM A61K038-54  
 ICS A61K038-46  
 IPCI A61K0038-54 [ICM,7]; A61K0038-46 [ICS,7]; A61K0038-43 [ICS,7,C\*]  
 IPCI-2 C12S0009-00 [ICM,7]; A61K0038-43 [ICS,7]  
 IPCR A61L0002-18 [I,C\*]; A61L0002-18 [I,A]; B08B0007-00 [I,C\*];  
 B08B0007-00 [I,A]; C02F0001-50 [I,C\*]; C02F0001-50 [I,A];  
 C12S0009-00 [I,C\*]; C12S0009-00 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 7 OF 13 USPTFULL on SIN DUPLICATE 2  
 AN 2003:37665 USPATFULL  
 TI Polypeptides having lactonohydrolase activity and nucleic acids encoding  
 same  
 IN Berka, Randy M., Davis, CA, UNITED STATES  
 Rey, Michael W., Davis, CA, UNITED STATES  
 PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.  
 corporation)  
 PI US 20030027310 A1 20030206  
 US 6756220 B2 20040629  
 AI US 2002-126170 A1 20020419 (10)  
 RLI Division of Ser. No. US 1999-434690, filed on 5 Nov 1999, GRANTED, Pat.  
 No. US 6395529 Continuation-in-part of Ser. No. US 1999-263041, filed on  
 5 Mar 1999, ABANDONED Continuation-in-part of Ser. No. US 1998-189497,  
 filed on 10 Nov 1998, ABANDONED  
 DT Utility  
 FS APPLICATION  
 LN.CNT 2289  
 INCL INCLM: 435/196.000  
 INCLS: 435/069.100; 435/320.100; 435/325.000; 536/023.200  
 NCL NCLM: 435/197.000; 435/196.000  
 NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200;  
 435/069.100; 435/325.000  
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 ICM C12N009-16  
 ICS C07H0021-04; C12P021-02; C12N005-06  
 IPCI C12N0009-16 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0021-02 [ICS,7]; C12N0005-06 [ICS,7]  
 IPCI-2 C12N0009-16 [ICM,7]; C12N0001-20 [ICS,7]; C12N0015-00 [ICS,7];  
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C02F0001-50 [I,C\*]; C02F0001-50 [I,A]; C12N0009-18 [I,C\*];  
 C12N0009-18 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 8 OF 13 USPTFULL on SIN DUPLICATE 3  
 AN 2002:148647 USPATFULL  
 TI 2,6-beta-D-fructan hydrolase enzyme and processes for using the enzyme  
 IN Moller, Soren, Holte, DENMARK  
 Johansen, Charlotte, Holte, DENMARK

Schafer, Thomas, Farum, DENMARK  
 Ostergaard, Peter Rahbek, Virum, DENMARK  
 Hoeck, Lisbeth Hedegaard, Skodsborg, DENMARK  
 PA Novozymes A/S, Bagsvaerd, DENMARK, DK-2880 (non-U.S. corporation)  
 PI US 20020076790 A1 20020620  
 US 6524827 B2 20030225  
 AI US 2001-969362 A1 20011002 (9)  
 RLI Division of Ser. No. US 1999-397885, filed on 17 Sep 1999, GRANTED, Pat.  
 No. US 6323007  
 PRAI DK 1998-1173 19980918  
 DK 1998-1623 19981209  
 US 1998-101615P 19980924 (60)  
 US 1998-111675P 19981210 (60)  
 DT Utility  
 FS APPLICATION  
 LN.CNT 3312  
 INCL INCLM: 435/200.000  
 INCLS: 435/069.100; 435/325.000; 435/320.100; 435/101.000; 536/023.200  
 NCL NCLM: 435/074.000; 435/200.000  
 NCLS: 435/183.000; 435/252.300; 435/252.330; 435/320.100; 536/023.200;  
 435/069.100; 435/101.000; 435/325.000  
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 ICM C12P019-44  
 ICS C07H021-04; C12N009-24; C12P021-02; C12N005-06  
 IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C\*]; C07H0021-04 [ICS,7];  
 C07H0021-00 [ICS,7,C\*]; C12N0009-24 [ICS,7]; C12P0021-02 [ICS,7];  
 C12N0005-06 [ICS,7]  
 IPCI-2 C12N0009-24 [ICM,7]  
 IPCR A61K0008-30 [I,C\*]; A61K0008-64 [I,A]; A61K0008-66 [I,A];  
 A61Q0011-00 [I,C\*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C\*];  
 A61Q0017-00 [I,A]; C11D0003-38 [I,C\*]; C11D0003-386 [I,A];  
 C12N0009-24 [I,C\*]; C12N0009-24 [I,A]; C12P0019-00 [I,C\*];  
 C12P0019-14 [I,A]; C12P0019-44 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 9 OF 13 USPATFULL on SIN DUPLICATE 4  
 AN 2002:60923 USPATFULL  
 TI Single-molecule selection methods and compositions therefrom  
 IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES  
 PI US 20020034757 A1 20020321  
 US 6762025 B2 20040713  
 AI US 2001-907385 A1 20010717 (9)  
 RLI Continuation of Ser. No. US 1998-81930, filed on 20 May 1998, GRANTED,  
 Pat. No. US 6287765  
 DT Utility  
 FS APPLICATION  
 LN.CNT 15716  
 INCL INCLM: 435/006.000  
 INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300  
 NCL NCLM: 435/006.000  
 NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500  
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 ICM C12Q001-68  
 ICS C07H019-00; C07H021-00; C07H021-02; C07H021-04; C12P019-34  
 IPCI C12Q0001-68 [ICM,7]; C07H0019-00 [ICS,7]; C07H0021-00 [ICS,7];  
 C07H0021-02 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*];  
 C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C\*]  
 IPCI-2 C12Q0001-68 [ICM,7]; C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C\*];  
 C07H0021-02 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C07H0021-00 [I,C\*]; C07H0021-00 [I,A]  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 10 OF 13 USPATFULL on STN  
 AN 2002:122473 USPATFULL  
 TI Polypeptides having lactonohydrolase activity and nucleic acids encoding same  
 IN Berka, Randy M., Davis, CA, United States  
 Rey, Michael W., Davis, CA, United States  
 PA Novozymes Biotech, Inc., Davis, CA, United States (U.S. corporation)  
 PI US 6395529 B1 20020528  
 AI US 1999-434690 19991105 (9)  
 RLI Continuation-in-part of Ser. No. US 1999-263041, filed on 5 Mar 1999, now abandoned Continuation-in-part of Ser. No. US 1998-189497, filed on 10 Nov 1998, now abandoned  
 DT Utility  
 FS GRANTED  
 LN.CNT 2055  
 INCL INCLM: 435/197.000  
 INCLS: 435/252.300; 435/320.100; 435/929.000; 536/023.200; 530/350.000  
 NCL NCLM: 435/197.000  
 NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200  
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 ICM C12N009-16  
 ICS C12N001-20; C12N015-00; C12N001-00; C07H021-04  
 IPCI C12N0009-16 [ICM,7]; C12N0001-20 [ICS,7]; C12N0015-00 [ICS,7];  
 C12N0001-00 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C\*]  
 IPCR C02F0001-50 [I,C\*]; C02F0001-50 [I,A]; C12N0009-18 [I,C\*];  
 C12N0009-18 [I,A]  
 EXF 435/197; 435/252.3; 435/320.1; 435/929; 536/23.2; 530/350  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 11 OF 13 USPATFULL on STN  
 AN 2001:214863 USPATFULL  
 TI 2,6- $\beta$ -D-fructan hydrolase enzyme and processes for using the enzyme  
 IN Moller, Soren, Holte, Denmark  
 Johansen, Charlotte, Holte, Denmark  
 Schafer, Thomas, Farum, Denmark  
 Ostergaard, Peter Rahbek, Virum, Denmark  
 Hoeck, Lisbeth Hedegaard, Skodsborg, Denmark  
 PA Novozymes A/S, Bagsvaerd, Denmark (non-U.S. corporation)  
 PI US 6323007 B1 20011127  
 AI US 1999-397885 19990917 (9)  
 PRAI DK 1998-1173 19980918  
 DK 1998-1623 19981209  
 US 1998-101615P 19980924 (60)  
 US 1998-111675P 19981210 (60)  
 DT Utility  
 FS GRANTED  
 LN.CNT 2422  
 INCL INCLM: 435/074.000  
 INCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100  
 NCL NCLM: 435/074.000  
 NCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100  
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 IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C\*]  
 IPCR A61K0008-30 [I,C\*]; A61K0008-64 [I,A]; A61K0008-66 [I,A];  
 A61Q0011-00 [I,C\*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C\*];  
 A61Q0017-00 [I,A]; C11D0003-38 [I,C\*]; C11D0003-386 [I,A];  
 C12N0009-24 [I,C\*]; C12N0009-24 [I,A]; C12P0019-00 [I,C\*];  
 C12P0019-14 [I,A]; C12P0019-44 [I,A]  
 EXF 536/23.1; 530/350; 435/183; 435/74; 435/200; 435/252.33; 435/262;  
 435/274; 435/320.1  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.



L3 ANSWER 12 OF 13 USPATFULL on STN  
 AN 2001:152673 USPATFULL  
 TI Methods for detecting and identifying single molecules  
 IN Cubicciotti, Roger S., Montclair, NJ, United States  
 PA Molecular Machines, Inc., Montclair, NJ, United States (U.S. corporation)  
 PI US 628/765 B1 20010911  
 AI US 1998-81930 19980520 (9)  
 DT Utility  
 FS GRANTED  
 LN.CNT 15456  
 INCL INCLM: 435/006.000  
 INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500  
 NCL NCLM: 435/006.000  
 NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500; 977/853.000  
 IC [7]  
 ICM C12Q001-08  
 ICS C12P019-34; C07M021-02  
 IPCI C12Q0001-08 [ICM,7]; C12Q0001-06 [ICM,7,C\*]; C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C\*]; C07M0021-02 [ICS,7]  
 IPCR C07H0021-00 [I,A]; C07H0021-00 [I,C\*]  
 EXF 435/6; 435/91.2; 536/22.1; 536/23.1; 536/24.3; 536/24.5  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 13 OF 13 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE009952 GenBank (R)  
 GenBank ACC. NO. (GBN): AE009952 AE013601-AE014015  
 GenBank VERSION (VER): AE009952.1 GI:22002119  
 SEQUENCE LENGTH (SQL): 4600755  
 MOLECULE TYPE (CI): DNA; circular  
 DIVISION CODE (CI): Bacteria  
 DATE (DATE): 2 May 2006  
 DEFINITION (DEF): *Yersinia pestis* KIM, complete genome.  
 SOURCE: *Yersinia pestis* KIM  
 ORGANISM (ORGN): *Yersinia pestis* KIM  
 Bacteria; Proteobacteria; Gammaproteobacteria;  
 Enterobacteriales; Enterobacteriaceae; *Yersinia*

COMMENT:

On or before May 2, 2006 this sequence version replaced  
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REFERENCE: 1 (bases 1 to 4600755)

AUTHOR (AU): Deng, W.; Burland, V.; Plunkett, G. III; Boutin, A.; Mayhew, G.F.; Liss, P.; Perna, N.T.; Rose, D.J.; Mau, B.; Zhou, S.; Schwartz, D.C.; Fetherston, J.D.; Lindler, L.E.; Brubaker, R.R.; Plana, G.V.; Straley, S.C.; McDonough, K.A.; Nilles, M.L.; Matson, J.S.; Blattner, F.R.; Perry, R.D.

TITLE (TI): Genome Sequence of *Yersinia pestis* KIM

JOURNAL (SO): J. Bacteriol., 184 (16), 4601-4611 (2002)

OTHER SOURCE (OS): CA 137:120475

REFERENCE: 2 (bases 1 to 4600755)

AUTHOR (AU): Deng, W.; Burland, V.; Plunkett, G. III; Boutin, A.; Mayhew, G.F.; Liss, P.; Perna, N.T.; Rose, D.J.; Mau, B.; Zhou, S.; Schwartz, D.C.; Fetherston, J.D.; Lindler, L.E.; Brubaker, R.R.; Plana, G.V.; Straley, S.C.; McDonough, K.A.; Nilles, M.L.; Matson, J.S.; Blattner, F.R.; Perry, R.D.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4600755	/organism="Yersinia pestis KIM" /mol-type="genomic DNA" /strain="KIM" /db-xref="taxon:187410"
gene	complement(21..461)	/gene="mioC" /locus-tag="y0001"
CDS	complement(21..461)	/gene="mioC" /locus-tag="y0001" /function="factor; DNA - replication, repair, restriction/modification" /note="residues 1 to 146 of 146 are 67.12 pct identical to residues 1 to 146 of 147 from E. coli K12 : B3742; residues 1 to 146 of 146 are 68.49 pct identical to residues 1 to 146 of 147 from GenPept : >gb AAL22733.1  (AE008881) initiation of chromosome replication [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="initiation of chromosome replication" /protein-id="AAM83597.1" /db-xref="GI:21956657" /translation="MADITLISGSTLGS AEYVAE HLADKLEEAGFSTEILHGFELDEL TLNGLWLI VITSTHGAGDLPDNLQPLLEQIEQQPK DLSQVRFGAVGLGSSEYDTFCGAI IKLDQQLIAQGAQRLGEILEIDVIQHEIPDPAE IWKVDWINLL" /gene="asnC" /locus-tag="y0002"
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coli K12 : B3743; residues 3 to
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to residues 2 to 152 of 152 from
GenPept : >emb|CAD03119.1|
(AL627280) regulatory protein
[Salmonella enterica subsp.
enterica serovar Typhi]"
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and gidA"
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TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS
TETLISLQNPIMRTIVE"
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coli K12 : B3745; residues 1 to
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to residues 1 to 483 of 483 from
GenPept : >dbj|BAB38110.1|
(AP002566) hypothetical protein
[Escherichia coli O157:H7]"

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WRVSLILQTIITIHQOLLEQEREQL
LAELQRRRLALSGALEPILTTNDNAAGRLWMSQG
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CDS       complement(3746..5299) /locus-tag="y0005"
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          residues 9 to 504 of 506 from E.
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          LILLKDCLWHDLNSFKLLQQQLEQLLTEQGYQQQ
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CDS       5573..7441 /locus-tag="y0006"
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          small molecules; cations"
          /note="residues 1 to 505 of 622

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are 83.96 pct identical to
residues 1 to 505 of 519 from E.
coli K12 : B3747; residues 1 to
622 of 622 are 84.72 pct identical
to residues 1 to 622 of 622 from
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(AE008881) KUP family, potassium
transport system, low affinity
[Salmonella typhimurium LT2]"
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transport system"
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organic acids, alcohols"
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VTF"
gene 8116..9042 /gene="rbsK"

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CDS	8116..9042	<pre> /locus-tag="y0008" /gene="rbsK" /locus-tag="y0008" /function="enzyme; degradation of small molecules; Carbon compounds" /note="residues 4 to 307 of 308 are 71.38 pct identical to residues 5 to 308 of 309 from E. coli K12 : B3752; residues 1 to 308 of 308 are 100.00 pct identical to residues 1 to 308 of 308 from GenPept : &gt;emb CAC88875.1  (AJ414141) ribokinase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="AAM83604.1" /db-xref="GI:21956664" /translation="METGKLVVLGSINADHILNI EQFPRPGETVIGQQYNVAFGGKGA NQAVAGRSGADIAFIACVGGDDDIGERVQQLTA DKIDTQPIEAIKGATTGVALIFVN SDGENVIGINAGANSAVTPEYLRRYQQQVIDADA LLMQLESPLDVTIAAAKLAKQHT QVILNPAPARKLPDELLTLVDMITPNETEAERLT GIHIEQDDDAKAAQILHDKGIAT VIITLGRGVWLSEQGGKRLVAGFKVNAVDTIAA GDTFNGALLTALLEGQSMDEVAVRF AHAHAALIAVTRPGAQPSIPWRAEIDSFLQERV" /locus-tag="y0009" /locus-tag="y0009" /note="residues 6 to 46 of 67 are 56.09 pct identical to residues 194 to 234 of 330 from GenPept : &gt;gb AAK16096.1 AF288084-2 (AF288084) NgrF [Phototribidus luminescens]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83605.1" /db-xref="GI:21956665" /translation="MSPVWQGYRQAMARAGLPPII AGYEVVSDFEFGGLVALKQRLNN PEAEPQVLPLTPELIERGSVSLR" </pre>
gene	9062..9265	
CDS	9062..9265	<pre> /locus-tag="y0010" /locus-tag="y0010" /function="putative transport" /note="residues 3 to 465 of 474 are 73.43 pct identical to residues 4 to 466 of 475 from E. coli K12 : B3754; residues 3 to 465 of 474 are 74.08 pct identical to residues 4 to 466 of 475 from GenPept : &gt;gb AAL22745.1  (AE008881) putative MFS family transport protein (1st module) [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="putative permease" </pre>
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NFVTIPGLVGPVMGPLLGLLLVTY
TTWHWIFILNPIGLLGIFYARKYMPNFTMPKRT
FDFVGFLFLFGISLVMISTSLIEMG
RPEIADYLPAAATLLGGLLMIFYIFHAKGHPNPL
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TGCVPFLMPLMLQVGFYSALAGCMMAPTAIGS
IMAKSAVTQVLRSLGYRKVLVGIT
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VLAVTQQLSISFGIAISATVLRFYDGLSLGGNVD
HFHYFITMGIVTLLSSLVFLLLK
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gene      complement(10766..11455 /locus-tag="y0011"
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CDS       complement(10766..11455 /locus-tag="y0011"
)

/note="residues 49 to 229 of 229
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coli K12 : B3755; residues 1 to
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to residues 1 to 229 of 230 from
GenPept :
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PQTNNYLDQELLTWMMTKENFDQ
VMOHFLILRTSLEPOACYLAATHANEKQRELLAS
LVAEMRALHSNFNREQWIQVDTQF
HKLIYEASGNPFLISFANFLSSVYYSYFRAITGD
EVIKLQHQNIQVDTILAGDNQGAAL
FACQVLLKTV"
gene      12016..13600
rRNA      12016..13600
/locus-tag="yr001"
/locus-tag="yr001"
/product="16S ribosomal RNA"
gene      13694..13766
tRNA      13694..13766
/locus-tag="yt001"
/locus-tag="yt001"
/product="tRNA-Glu"
/note="anticodon: TTC"
gene      14022..16928
rRNA      14022..16928
/locus-tag="yr002"
/locus-tag="yr002"
/product="23S ribosomal RNA"
gene      complement(17019..17426 /locus-tag="y0012"
)
CDS       complement(17019..17426 /locus-tag="y0012"
)

/note="residues 48 to 120 of 135

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are 30.00 pct identical to
residues 84 to 159 of 443 from
GenPept :
>gb|AAD36903.1|AE001821-3
(AE001821) hypothetical protein
[Thermotoga maritima]"
/codon-start=1
/transl-table=11
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/translation="MDGLSVYLIPGSVLLSHGET
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CRQVNSFLLLPNLIHVTGADTQSRGDLTLTKGA
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/locus-tag="yr003"
/locus-tag="yr003"
/product="5S ribosomal RNA"
gene 17036..17155 /locus-tag="yt002"
rRNA 17036..17155 /locus-tag="yt002"
/product="tRNA-Thr"
gene 17169..17241 /note="anticodon: GGT"
tRNA 17169..17241 /locus-tag="yr004"
/locus-tag="yr004"
/product="5S ribosomal RNA"
gene 17285..17399 /gene="metA"
rRNA 17285..17399 /locus-tag="y0013"
/locus-tag="y0013"
gene 18140..19069 /gene="metA"
CDS 18140..19069 /locus-tag="y0013"
/function="enzyme; amino acid
biosynthesis: Methionine"
/note="residues 1 to 309 of 309
are 79.61 pct identical to
residues 1 to 309 of 309 from E.
coli K12 : B4013; residues 1 to
309 of 309 are 79.61 pct identical
to residues 1 to 309 of 309 from
GenPept :
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(AE005633) homoserine
transsuccinylase [Escherichia coli
O157:H7 EDL933]"
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/transl-table=11
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transsuccinylase"
/protein-id="AAM83609.1"
/db-xref="GI:21956670"
/translation="MPIRVPELPAVSFLRNENV
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PKKIETENQFLRLSNSPLQVDIQLLRVDSRESK
NTPTEHLNFFYCDFEDIQDNQFDG
LIVTGAFLGLVDFCDVAYWPQIERIIAWAKEHVT
STLFVCWAVQAALNILYGIPKMTIR
EVKLSGIYQHQTLEPLALLTRGDETFLAPHSRY
ADFPVEVLQOYTDLIDILVSSEEAG
AYLFASKDKRVAFTVGHPEYDVDDTLAGEYQRDLA
AGLNPQVPLNYFPSDDASLRPKAS
WRSHGHLLEFANWLNYYVYQITPFDLRHMNPTLD"
gene complement(19262..19411 /locus-tag="y0014"
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CDS      complement(19262..19411 /locus-tag="y0014"
)
        /note="residues 7 to 48 of 49 are
        33.33 pct identical to residues
        512 to 553 of 1005 from GenPept :
        >gb|AAK39925.1|AF165818-133
        (AF165818) hypothetical protein
        [Guillardia theta]"
        /codon-start=1
        /transl-table=11
        /product="hypothetical"
        /protein-id="AAM83610.1"
        /db-xref="GI:21956671"
        /translation="MSLPVKKAEFYGYFSPDRNK
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gene      19456..21087
CDS      19456..21087
        /gene="aceB"
        /locus-tag="y0015"
        /gene="aceB"
        /locus-tag="y0015"
        /function="enzyme; central
        intermediary metabolism:
        Glyoxylate bypass"
        /note="residues 12 to 543 of 543
        are 79.54 pct identical to
        residues 1 to 533 of 533 from E.
        coli K12 : B4014"
        /codon-start=1
        /transl-table=11
        /product="malate synthase A"
        /protein-id="AAM83611.1"
        /db-xref="GI:21956672"
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        ETNSIRDGDW*KIQQIPADLRDRRV
        EITGPVERKMYINALNANVKVMADFEDSLAPSW
        DKVIDGQINLHDAVKGTISYTNES
        GKVYQLKPNPAVLARVRGLHLPKHKVWKQDEAI
        PGGFLDFALYFYHNYQQLLAKGSG
        PYFYLPMKMSYQEAAWSDVFNFTEQRFGLSQGT
        IKATVLIETLPVAFQMDIILYHLR
        HHIVGLNCRWDYIFSYIKTLKNHPDRVLPDRQS
        VTMNKPFLSAYSRLIKTCHKRGA
        LAMGGMAAFIPDKDAEKNKLVLDKVRADKELEAS
        NGHDGTWVAHPGLADTVMDVFNKV
        LGSRPNQLEVSREQDKPITAALLEPESGTEREA
        GMRANIRVAVQYIEAWISNGGCVF
        IYGLMEDAATAEISRTSIWQWIHHQKSLNSGQTV
        TKELFRSMLSEEIQVVKLEGAER
        FDRGRFEEAARLMERITTQDELIDFLTLPGYALL
        A"
        /gene="aceA"
        /locus-tag="y0016"
        /gene="aceA"
        /locus-tag="y0016"
        /function="enzyme; central
        intermediary metabolism:
        Glyoxylate bypass"
        /note="residues 4 to 435 of 435
        are 85.18 pct identical to
        residues 3 to 434 of 434 from E.
        coli K12 : B4015; residues 1 to

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gene 22514..24241  
CDS 22514..24241

435 of 435 are 100.00 pct  
identical to residues 1 to 435 of  
435 from GenPept :  
>emb|CAC93193.1| (AJ414158)  
isocitrate lyase [Yersinia  
pestis]"  
/codon-start=1  
/transl-table=11  
/product="isocitrate lyase"  
/protein-id="AAM83612.1"  
/db-xref="GI:21956673"  
/translation="MTISRTQQIQLEQEWTSR  
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LQQAAGVEAIYMSGWQVAADANT  
ASSMYPDQSLYPVDSVPAVVKRINNSFRADQIQ  
WSNNIEPGSKGYTDYFLPIVADAE  
AGFGGVLNFAFELMKAMIEAGAAGVHFEDQLAAVK  
KCGHMGKVLVPTQEAIQKLVAAR  
LAADVGLGVPTLLIARTDADAADLLTSDCDPYDRE  
FITGDRTAEGFFRTRAGIEQAISR  
GLAYAPYADLVWCETSTPDLALAKRFADAVHAQF  
PGKLLAYNCSPSPFNWKNLTDQOI  
ASFQDELSAMGYKYQFITLAGIHSMMWFNMFDLAH  
AYAQEGMKHYVEKVQQPEFASVD  
RGYTFASHQQEVGIGYFDKVTNIIQGGASSVTAL  
TGSTEEQQF"  
/gene="aceK"  
/locus-tag="y0018"  
/gene="aceK"  
/locus-tag="y0018"  
/function="enzyme; central  
intermediary metabolism:  
Glyoxylate bypass"  
/note="residues 5 to 572 of 575  
are 75.52 pct identical to  
residues 5 to 572 of 578 from E.  
coli K12 : B4016; residues 5 to  
572 of 575 are 75.88 pct identical  
to residues 5 to 572 of 578 from  
GenPept :  
>gb|AAG59208.1|AE005633-5  
(AE005633) isocitrate  
dehydrogenase kinase/phosphatase  
[Escherichia coli O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
/product="isocitrate dehydrogenase  
kinase/phosphatase"  
/protein-id="AAM83613.1"  
/db-xref="GI:21956675"  
/translation="MVAKLEQLIAQTILQGFDAG  
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LARVKEIYTGLLPDYPRFEIAESF  
FNSVYCRFLFKHRDLTPDKFLVFSSQPERRFREIP  
RPLARDFIPKGDLSGMLQMVNLNDL  
SLRLHWENLSRDIDYIVMAIRQAFTDEQLASAHF  
QIANELFYRNKAAWLVGKLRNLGD  
IYFLLPIHHNESGELFIDTCLTSKAEASIVFGF  
ARSTFMVYVPLPAAWVWLRLEILP  
GKSTAELYTAIGCQKHGKTESYREYLAFIHQSSE

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QFIIAPGVKGMVMLVFTLPSFDRV
FKVIKDQFAPQKEVTQARVLECYQLVKEHDRVGR
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LQHEVPEKLEDLGDKIVIKHLYMERRMTPLNLYM
EQADDQQLKDAIEYGNAIKQLAA
ANIFPGDMLFKNFGVTRHGRVVFYDYDEICYMTE
VNFIRDIPPPRYPEDEMASEPWYSV
SPNDVQPEEFRRHFLCDRQVRHFFEMHGDLFQA
SYWRGLQQRRIRDGHVDFVFAYRRK
QRFSQLALN"
gene      complement(24077..24214 /locus-tag="y0017"
)
CDS       complement(24077..24214 /locus-tag="y0017"
)
/note="residues 1 to 39 of 45 are
35.89 pct identical to residues
160 to 198 of 460 from GenPept :
>gb|AAF52902.1| (AE003628) CG13138
gene product [Drosophila
melanogaster]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83614.1"
/db-xref="GI:21956676"
/translation="MLSSISKNILHMPIDTLLQ
AAPITGLEQIAVHLLKKVPDFPVT A"
gene      complement(24361..24954 /gene="ic1R"
)
CDS       complement(24361..24954 /locus-tag="y0019"
)
/gene="ic1R"
/locus-tag="y0019"
/function="regulator; central
intermediary metabolism:
Glyoxylate bypass"
/note="residues 5 to 192 of 197
are 78.19 pct identical to
residues 98 to 285 of 287 from E.
coli K12 : B4018"
/codon-start=1
/transl-table=11
/product="repressor of aceBA
operon"
/protein-id="AAM83615.1"
/db-xref="GI:21956677"
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LLAMVHPMLRRLMDESGETVNLAV
LDHSDYQAI IIDQVQCTALMRMSAPIGGKLPMAH
SGAGKAFSLSTLPDDQLVQLLHKKG
LHAYTOHTRTNPTSLKENLALIRKQGYSFDDDEEH
ALGLRCIAACLFDEHHEAFAAISII
SGPISRITDDRVTELGA LVIHAAKEITQSYGGGT
GVK"
gene      25420..29115 /gene="meth"
CDS       25420..29115 /locus-tag="y0020"
/gene="meth"
/locus-tag="y0020"
/function="enzyme; amino acid
biosynthesis: Methionine"
/note="residues 6 to 1231 of 1231
are 85.90 pct identical to

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residues 1 to 1227 of 1227 from E.  
 coli K12 : B4019; residues 6 to  
 1231 of 1231 are 86.14 pct  
 identical to residues 30 to 1256  
 of 1256 from GenPept :  
 >gb|AAL23012.1| (AE008895)  
 B12-dependent  
 homocysteine-N5-methyltetrahydrofo  
 late transmethylase, repressor of  
 metE and metF [Salmonella  
 typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="B12-dependent  
 homocysteine-N5-methyltetrahydrofo  
 late transmethylase, repressor of  
 metE and metF"  
 /protein-id="AAM83616.1"  
 /db-xref="GI:21956678"  
 /translation="MVDITVDINKVKELHQQLAQR  
 ILVLDGGMGTMIQSYRLEEADYRG  
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 AGADILETNTTFNSTSIAMADYQMA  
 SL\$AEINYEAAARLARICADEWSARTPEKPRIVAG  
 VLGPTNRTASISPKVNDPAFRNV  
 FDQLVEAYRESTRALIEGGVDLIMIETVFDTLNA  
 KAATFAVESEFEVMGVLLPVMISG  
 TITDASGRTLSGQTTEAFYNSLRHVKPLSFG LNC  
 ALGPDELQYVAELSRISYEYVSA  
 HPNAGLPNAGFGEYDLEAKEMAEQIGEWARAGFLN  
 IVGGCCGTTTPRHIAAMVNAVAGVP  
 PRPLPDIPVACRLAGLEFLTIDANTL FNVNGERT  
 NVTGSARFKRLIKEKYGEALDVA  
 RQOVESGAQIIDINMDEGMLDAEAMVRFLNLIA  
 GEPDIARVPI MIDSSRWVIEKGL  
 KCIQKGIVNSISMKEGVDAFIHHA KLVRRYGAA  
 MVMMAFDETGQADTRARKIEICRR  
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 VSNVSFSFRGNDPVEA IHAVFLYYAIRNGMDMG  
 IVNAGQLAIYDDLSD ELRDAVEDV  
 ILNRRDDSTERLLDLAEKYRDSKSGEVAIQAEW  
 RGWPVVKRLEYSLVKGIT EFIELD  
 TEEARQQADRP IEVIEGFLMSGMNVVGD LFGEGK  
 MFLPQVKSARVMQAVAYLEPYI  
 EASKQKGT TAGKILLATVKGVDHIGKNIGVV L  
 QCNNY EIIDLGMVPT EKI LRTAR  
 EEKVDI IGLSGLITPSLDEMNVNAKEMERQGF TL  
 PLLIGGATT SKAHTAVKIEQNYSG  
 STTYVSNASRSVGVVSALLSDTQREAFVAKTRKE  
 YETVRIQHARKKPRTPPVSLQAAR  
 NNPTVIDWENYTPPVAHKLGVOQVVEAS IETLRNY  
 IDWTFPFMTWSLAGKYPRILEDEV  
 VGEEAKRLLADANALLDKLSAEDLLHPKGVVGLF  
 PANSVGGDDIEIYRDERRDEVLAIS  
 YHLRQQTEKTD FPNYCLADYVAPKSSGKADYFGA  
 FAVTGGLEEDALADAYDAQHDDYN  
 KIMIKALSDRLAEAFAYELHERVRKVYWG FAPNE  
 NLSNEELVRENYQGIRPAPGPAC  
 PEHTEKGQIWLQLLDVETHTGMKLTESYAMWPGAS  
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gene      complement(29211..34175 /gene="hyla"
)
/locus-tag="y0021"
CDS      complement(29211..34175 /gene="hyla"
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/function="putative factor;
extracellular functions; secreted
proteins"
/notes="residues 20 to 1651 of 1654
are 42.08 pct identical to
residues 1 to 1604 of 1608 from
GenPept : >gb|AAA50323.1| (M22618)
hemolysin [Serratia marcescens]"
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ATSAGNSILAGQLAANQNLNGQAASIIILNEVISR
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GITCNGCGFMNTNRESLVVGNPLIEQGSILKGFET
FNNNNWLI IQDKGLTANKILDLIA
PRIEVTGMVTS EAINALSGNNQISTDGGQILESR
QEDHPNRPRTSLGGWFSLSFSSESE
ESIDGKYLGSMSQGRINLVSTREGSGVKIAGSLN
GSEINATIKGLQLEAAKLGND
ININANSIQAFGNLHKNEEDNGGVTSQSLERTQLKG
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DGNILISVKDDVAITGSKVKATKD
GFVQAKEGGIKIDNAISTTNKVDERTGVAFDIT
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KIISKDQDVIGSLVKSAGELGIETLGDINVA
AEQKQKIDQKTLTTIDGFTSDDGK
NQYQAGLKVEHTSESEKTEKVINHGSTLEGTVK
LEADKDVTF TGSQNLNTTKGDADIT
AENVSFVAAQDTTTSNKEKETGVNAHYTGGMDK
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HTDVKGDNLNNAKQEI TNQGT DHNVEGSYAANAT
NVNNLAENSETTTTTTNTVDVKY
GGNIA YDGVTRPVEKTI ES GKKLDVGGVIE NVGN
VAPDSVNAGVDLSVNVGEKENKSS
NSQAVVTSIKSGDISITAKEDVKDQGTHYQADKG
GIKIDAAHHTFESAVNRAEESKV
VSGGVD MRYTTTGEDINVDAGKKGKNGKQEVKA
EQAQTGSMKAVGDI I INVQENARY
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GTKTHTNNKGSAGAEANVKNTDE  
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 GVEEQSAIRGTQNVDLTVKGKTDLVGGKISSKNS  
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gene      complement(34188..35964 /locus-tag="y0022"
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                                     /note="hylB; disrupted by
                                     frameshift"
                                     /pseudo
gene      complement(36445..37830 /gene="lysC"
)
                                     /locus-tag="y0023"
CDS       complement(36445..37830 /gene="lysC"
)
                                     /locus-tag="y0023"
                                     /function="enzyme; amino acid
                                     biosynthesis: Lysine"
                                     /note="residues 14 to 461 of 461
                                     are 81.47 pct identical to
                                     residues 2 to 449 of 449 from E.
                                     coli K12 : B4024; residues 14 to
                                     461 of 461 are 81.47 pct identical
                                     to residues 2 to 449 of 449 from
                                     GenPept :
                                     >gb|AAG59223.1|AE005635-3
                                     (AE005635) aspartokinase III,
                                     lysine sensitive [Escherichia coli
                                     O157:H7 EDL933]"
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                                     /protein-id="AAM83618.1"
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                                     MLENIAMLSEAASLATSPALTDLVSHGELMSTL
                                     LFVELLRQRQVAWEVFDVRKVMRT
                                     NDRFGRAEPDTSALAELAQTLLAPRIEDAIVVTQ
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                                     DKIAFEAAEMATFGAKILHPATL
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                                     FRALALRRKQTLTLLHSLNMLHAR
                                     GFLAEVFNILARHSISVDLITTSVSVALTLDTT
                                     GSTSTGDSLLTTSLLTELSSLCRV
                                     EVEEDLALVAIIGNLNSQACGVGKEVFGVLPDPFN
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gene	38200..39846	/gene="pgi"
CDS	38200..39846	/locus-tag="y0024"
		/gene="pgi"
		/locus-tag="y0024"
		/function="enzyme; energy metabolism, carbon: Glycolysis"
		/note="residues 1 to 548 of 548 are 87.40 pct identical to residues 1 to 548 of 549 from E. coli K12 : B4025; residues 1 to 548 of 548 are 87.40 pct identical to residues 1 to 548 of 549 from GenPept : >gb AAG59224.1 AE005635-4 (AE005635) glucosephosphate isomerase [Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="glucosephosphate isomerase"
		/protein-id="AAM83619.1"
		/db-xref="GI:21956682"
		/translation="MKNINPQSQTAAWKALQQHFE QMKDVTISSLFAKDDQRFNRFSAT FDDQMLVDFESKNRITSETLEKLQDLAKETDLA GIKSMFSGEIKNRTEGRAVLHIALR NRSNTPIVVDGKDVMEVNAVLAQMKQFCDRVIS GDWKGVTGKAITDVVNIGIGGSDL GPYVTEALRPYKNHLNMHFSNVVDGTHIAEAL PLNPETTLFLVASKTFTTTQETMTN AHSARDWFLSAAGDPAHVAKHFAALSTNAKAVGE FGIDTNNMFEFWDWVGGYSLWSA IGLSIALSVGFEHFEQLLSGAHAMDKHFAETPAE KNLVLLALIGIWNFFGAETEA ILPYDQYMHRRFPAYFQQGNMESNGKYVDRNGHPV DYQTGPPIIWGEPGTNGQHAFYQLI HQGTLKIPCDFIAPAISHNPLSDHHAKLLSNFFA QTEALAFGKSLEDVEAEFAAAGKT PEQVAHVAPFKVFEGNRPTNSILLREITPFSLGA LIALYEHKIFTQGVILNIYTFDQW GVELGKQLANRILPELADDQEVTSHDSSSTNALIN RFKNWR"
gene	39981..40388	/locus-tag="y0025"
CDS	39981..40388	/locus-tag="y0025"
		/note="residues 6 to 135 of 135 are 67.69 pct identical to residues 8 to 136 of 136 from E. coli K12 : B4030"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83620.1"
		/db-xref="GI:21956683"
		/translation="MAKNSRSQWIAKNLQRLNVL GLIMLAAILVVFLVKETIHLGKVL FLSNQETSSYMLIEGIVIFYFLYEFIALIVKYFE SGYHFPPLRYFIYIGITAIIRLIIV DHENPIDTLIYSGSILVLVVTLYLANTERLKRE"
gene	complement(40531..41442)	/gene="malG"
	)	/locus-tag="y0026"



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CDS      complement(40531..41442 /gene="malG"
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        /locus-tag="y0026"
        /function="transport; transport of
        small molecules; carbohydrates,
        organic acids, alcohols"
        /note="residues 8 to 303 of 303
        are 88.17 pct identical to
        residues 1 to 296 of 296 from E.
        coli K12 : B4032; residues 8 to
        303 of 303 are 90.87 pct identical
        to residues 1 to 296 of 296 from
        GenPept : >gb|AAL23051.1|
        (AE008897) ABC superfamily
        (membrane), maltose transport
        protein [Salmonella typhimurium
        LT2]"
        /codon-start=1
        /transl-table=11
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        transporter"
        /protein-id="AAM83621.1"
        /db-xref="GI:21956684"
        /translation="MTKEEMQMAMVQPKSQRLRL
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        GSVTPPPFPFVMLWLWNSIKIALIT
        AMGIVALSTTCAYAFARMRFRGKSALLKGLIFQ
        MFPAVLSLVALYALFDRIGQYMF
        IGLNTHGGVIFAYMGGIALHVWTIKGYFETIDNS
        LEEAAALDGATPQWQAFRLVLLPLS
        VPILAVVFILSFIAAITEVPVASLLLRDVNSYTL
        AVGMQQYLNPNQNYLWGDFAAAVL
        SAIPITTVFLLAQRWLVGGLTAGGVKG"

gene      complement(41435..43027
)
        /locus-tag="y0027"
        /gene="malF"

CDS      complement(41435..43027
)
        /locus-tag="y0027"
        /function="transport; transport of
        small molecules; carbohydrates,
        organic acids, alcohols"
        /note="residues 18 to 530 of 530
        are 75.43 pct identical to
        residues 5 to 514 of 514 from E.
        coli K12 : B4033"
        /codon-start=1
        /transl-table=11
        /product="inner membrane permease
        of maltose ABC transporter"
        /protein-id="AAM83622.1"
        /db-xref="GI:21956685"
        /translation="MKGNIQMSHTELQSRKKKI
        AWWQSDALKWLVISLLSLFTCYLI
        VLMYAQGEYLFIAIVTILVSLGLYVFANRRAYAW
        RYVYPGVAGMGLFVLFPLICTIAI
        AFTNYSSTNQLTFERAQSVLLDRQFQTGKTFTFG
        LYPSDNQWRLQLTNPDGSLFISE
        PFSEATGEQKVMVAPTNTAQTSEPASLRITQS
        RQALSSLVAILPDGAELRMSSLRQ

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gene 44998..45234  
CDS 44998..45234

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/codon-start=1
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/product="hypothetical"
/protein-id="AAM83624.1"
/db-xref="GI:21956687"
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RDGQNGVG DYRGLNGVCDSL LFC
WISMLRRCITCS PILRPRRRPGQPCHWLGGTARS
ERVIRALGVINGSCRGLLPLFFFFI
QIHMKSLRKQRSNAWLM"
/locus-tag="y0029"
/locus-tag="y0029"
/note="residues 33 to 76 of 78 are
34.78 pct identical to residues
399 to 444 of 933 from GenPept :
>gb|AAG51093.1|AC025295-1
(AC025295) auxin response factor 6
(ARF6) [Arabidopsis thaliana]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83625.1"
/db-xref="GI:21956688"
/translation="MRLIITLLDQYVEALFNVQP
YTQAATPSGATILPLAWRHGAQRES
HQGTGGNQWVMPGFASTVFLHSDSYEKLFAQAKE
"
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gene 45238..46347  
CDS 45238..46347

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/gene="malK"
/locus-tag="y0031"
/gene="malK"
/locus-tag="y0031"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 1 to 369 of 369
are 84.90 pct identical to
residues 1 to 371 of 371 from E.
coli K12 : B4035; residues 1 to
369 of 369 are 84.55 pct identical
to residues 1 to 369 of 369 from
GenPept : >gb|AAL23054.1|
(AE008897) bifunctional: ABC
superfamily (atp-bind), maltose
transportprotein; phenotypic
repressor of mal operon
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="ATP-binding component of
ABC transport system for maltose"
/protein-id="AAM83626.1"
/db-xref="GI:21956689"
/translation="MANVTLLSSVYKAFGEAVISR
DINLEIDDGEFVVFVGPSCGKST
LLRMIAGLEDITS GELLIGKRMNEVPPSERGIG
MVFQSYALYPHLSVAENMSFGLKL
AGVKKAEIYQRVNVQAEVLQLAHLDDRPKALSG
GQRQVIAIGRTLVS EDPVFLLED
LSNLDAALRVQMRIEISRLHKRLERTMIYVTHDQ
VEAMTLADKIVVL DAGNIAQVGKP
LELYHY PANRFVAGF IGSPKMNFLPVKVTAAEPR
QVQIELPNHQRVVLPVEGDQVQVG"
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		ANMSLGIRPEHLLPSSASEVTLEGEIQVVEQLGN ETQIHQIPAIRQNLVYRQNDVVL VEEGATFSIGLPPHRCFLFREDGTACKRLYQELG y"
gene	46250..47689	/gene="lamB" /locus-tag="y0032"
CDS	46250..47689	/gene="lamB" /locus-tag="y0032" /function="transport of small molecules; carbohydrates, organic acids, alcohols" /note="defective for phage lambda uptake; residues 83 to 475 of 479 are 87.96 pct identical to residues 2 to 400 of 400 from GenPept : >gb AAA70348.1  (U16150) maltoporin [Yersinia enterocolitica]" /codon-start=1 /transl-table=11 /product="maltose high-affinity receptor" /protein-id="AAM83627.1" /db-xref="GI:21956690" /translation="MQHSPSVCHRIGVTSSVRMA LHVSGETKNWASSYGDAWLQRMKA RMPITGKYNRRLLMITLRKLPALAVAAGVLSTQA MAVDFHGYARSGIGWTASGGEQQC FQTITGAQSKYRLGNECETYAELKQELWKEGDK SFYLDTNVAYSVSQRDDWESTDPA FREANVQGNLIESLPGSTIWAGKRFYQRHDVHM IDFYWDISGPGAGLETIDLGFCK LSVAATRNSESAGSSAWINDQRENAKYTINNVDY VRLAGLETNPGGSLELGVDYGRAD TQEGYSLAPNASKDGVMLTAEHTQSLMGGFNKFV VQYATDSMTSYNTGHSQGTSVNNN GHLLRVIDHGAINLAEKWDMMYVALYQDIDLNN NGNTWYSVGVPRMYKWTPI MSTLL EAGYDNVKSQHTGERNGQYKLLAQQWQAGDSIW SRPAIRVFATYANWDEKGYSDTT GVAQDGTIGTNSRGKNNEVTFGAQFEAWW"
gene	47912..48841	/gene="malM" /locus-tag="y0033"
CDS	47912..48841	/gene="malM" /locus-tag="y0033" /function="phenotype; degradation of small molecules; Carbon compounds" /note="residues 7 to 309 of 309 are 51.80 pct identical to residues 3 to 306 of 306 from E. coli K12 : B4037; residues 7 to 309 of 309 are 50.98 pct identical to residues 3 to 305 of 305 from GenPept : >gb AAL23056.1  (AE008898) periplasmic protein of mal regulon [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="periplasmic protein of mal regulon"

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/protein-id="AAM83628.1"
/db-xref="GI:21956692"
/translation="MYEGITMKKNLLSLCLVLAL
GGTAPLAVQAASTISPANVSIAPT
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EVEGAVAAAFALPADRGSLVLTSS
LLTDKQLFTPSVLVLDEQMRPAAYFPSSYFTYEK
AGIMINDRLQGVMKLTLPALGQKQI
YLLVYTTTRDDLKKTQLLDDPAKAYAQQGVGNAVPD
IPDPVNVHSPGTGLRIKVTSEQGM
GNIMIGLIQSAPTSAPVVGSSIQPVAAPQSEPA
KPAAPMLGETENYFNQAIKDAVKA
GDVDKALKLLNEAEHLGSTSARKTFIGSVKGGK"

gene      complement(49078..49236
)
CDS       complement(49078..49236 /locus-tag="y0034"
)

/note="residues 5 to 52 of 52 are
34.00 pct identical to residues
508 to 557 of 597 from GenPept :
>gb|AAF30492.1|AE002108-5
(AE002108) DNA polymerase III
gamma-tau subunits [Ureaplasma
urealyticum]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83629.1"
/db-xref="GI:21956693"
/translation="MTKKVAIIGVVNLFIDVTHL
CINKYCKSFSLCSQIPIERKPNL NVILNKKE"

gene      49240..49590
CDS       49240..49590
/locus-tag="y0035"
/locus-tag="y0035"

/note="residues 37 to 95 of 116
are 39.39 pct identical to
residues 12 to 74 of 476 from
GenPept : >emb|CAC05244.1|
(AL391604) DNAJ domain protein
similar to human tetratricopeptide
repeat protein and protein kinase
inhibitors [Schizosaccharomyces
pombe]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83630.1"
/db-xref="GI:21956694"
/translation="MTLNMGTGSSLVVEKNPVGNF
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RELKTHLICNEFVKNSKIVTVYITLGNDAALLI
YYSNRVIFYKSYIKGDIACMNYT
VNEGYLTTEILWR"

gene      complement(49742..50260 /locus-tag="y0036"
)
CDS       complement(49742..50260 /locus-tag="y0036"
)

/note="residues 1 to 172 of 172
are 80.23 pct identical to
residues 1 to 172 of 172 from
GenPept :
>gb|AAG54535.1|AE005199-5
(AE005199) Z0266 gene product

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[Escherichia coli O157:H7 EDL933]"
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protein"
/protein-id="AAM83631.1"
/db-xref="GI:21956695"
/translation="MPTPAYISITGKTQGNITAG
AFTAESVGNIIYVQGHEDMLVQEF
EHIVTVPTDPQSGQPSGQRAHKPLRFTVAYNKAV
PLLNALASGEMLPTVELKWKYRTS
IEGQEHFFTTKLEDATIIDICKMPHCQDSTKA
EFTQLVRVSLAYRKINWDHTTAGT
SGADDWRAPIEA"
gene      50781..51281
CDS       50781..51281
/locus-tag="y0037"
/locus-tag="y0037"
/notes="residues 2 to 166 of 166
are 62.65 pct identical to
residues 1 to 166 of 166 from
GenPept :
>gb|AAG54533.1|AE005199-3
(AE005199) Z0264 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAM83632.1"
/db-xref="GI:21956696"
/translation="MMSKNKQSSVAPKERINIKY
VPNTGDQVAEIELPLNLVVVDLKG
GVREETSIEERQVVSVNKNFNFSVMNEANISLSF
NVPNRLEGDEEDMPVALSIKGLD
DFSPDNVAKKVPKLELREALVALKGPLGNI
PAFRSRLQDLLGNEDMREQLLKEI DIINQK"
gene      51349..52830
CDS       51349..52830
/locus-tag="y0038"
/locus-tag="y0038"
/notes="residues 20 to 492 of 493
are 76.95 pct identical to
residues 19 to 491 of 492 from
GenPept : >gb|AAF96022.1|
(AE004353) conserved hypothetical
protein [Vibrio cholerae]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83633.1"
/db-xref="GI:21956697"
/translation="MPLHEENTVLAEPASATFL
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LVDRDTFRENKINIMHATKEELLEDFEFSPEII
QSGFYKHVYSSGYGQFGGEPAAI
IGNYAFNNSSPDMKLLQYVSAGVAMAHAPFLSSV
APDFFGISSTFELPAIKDLKSVFE
GPAHTKWRALRESEDSRYLGLTTPRFLRLPYST
VENPIKNFNYYEDVRNHEHFLWG
NTAFLLASCLTDSFAKYRWCNPNIIGPQSGGIVHD
LPVHLIYEAQMGIQAKIPEVLITD
RREFELAEEGFITLTKRKGSDNAFFSANSVQKP
KVFPNTREGKMAETNYKLGTLQLPY

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MFVINRLAHYIKVLQREQIGSWKERQDLERELNI
WLKQYIADQENPPTDVRSSRRLRS
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SLVGRLDKE"
gene      52837..53277      /locus-tag="y0039"
CDS       52837..53277      /locus-tag="y0039"
                               /note="residues 11 to 140 of 146
                               are 35.8% pct identical to
                               residues 8 to 134 of 137 from
                               GenPept :
                               >gb|AAG54530.1|AE005198-11
                               (AE005198) Z0261 gene product
                               [Escherichia coli O157:H7 EDL933]"
                               /codon-start=1
                               /transl-table=11
                               /product="hypothetical"
                               /protein-id="AAM83634.1"
                               /db-xref="GI:21956698"
                               /translation="MAALLNWRGSSASLFDRIQ
                               KGKASSSSDGLRRELLNSIQKHLN
                               EVLNSRPGACQSAVDLGVIDLNDATATSSDFRKS
                               IEKAIKDCIENYEPRISAVTVQSL
                               LNHGDPLQLSFHISARVNFDDMGDVVEFNIQLDN
                               NRRYCFNQET"
gene      53277..54503
CDS       53277..54503      /locus-tag="y0040"
                               /locus-tag="y0040"
                               /note="residues 4 to 365 of 408
                               are 49.58 pct identical to
                               residues 5 to 367 of 616 from
                               GenPept :
                               >gb|AAG54529.1|AE005198-10
                               (AE005198) Z0260 gene product
                               [Escherichia coli O157:H7 EDL933]"
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                               /transl-table=11
                               /product="hypothetical"
                               /protein-id="AAM83635.1"
                               /db-xref="GI:21956699"
                               /translation="MSFEKYFRDEL DYLRQLGRD
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                               LEGFAFLTGNLREKIDDOFPELTGLLNMLWPNY
                               LRPIPSMTIIEYTPDESUVVTEATL
                               VKRGSQVMISPIAQNGQSAFINSNAHAGPQCTF
                               TILCRD VWLFPMISIREISANSSNEQ
                               GILSIHFAAKAELNLQDLQDLKRLFYLGEDNYTS
                               TQLYFWINHYFERAELVVGITIP
                               MPDFFDNVPVGFERDDALLPYPKNAYMGYRILQEY
                               FCFPEGFLFFDVGNGVVDFFPHLNA
                               SEFSLNLYFSQALPPEVKVRSTTLRMNCTPAVN
                               LFOHDSEAIDLGTQTEYPLCVSYH
                               NPDHYDIFSVDRVDSWLSEKGVKPKGRGRALNPKT
                               WTSALLFLYLSPVFCRTHSACFQA
                               NALCIVIMDIFYNVTL"
repeat-region complement(54361..54622) /note="insertion element; partial"
)
)
gene      complement(54393..54650) /insertion-seq="IS1661"
)      /locus-tag="y0041"
CDS       complement(54393..54650) /locus-tag="y0041"
)
)
/function="IS and transposon
related functions"

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/feature="IS1661 orfB; residues 5 to
84 of 85 are 60.49 pct identical
to residues 158 to 238 of 240 from
GenPept : >emb|CAA63547.1|
(X92970) orfB [Escherichia coli]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83636.1"
/db-xref="GI:21956700"
/translation="MDHFSSVVDRIQSMSRKGN
CLDNAVMENFFSHLKAEMYHKKY
DSATVLKRDIIVEYIHYYNTERISLKTGGMSPAEY
RTQVEKQ"
repeat-region complement(54623..56576 /note="insertion element"
)
)
/insertion-seq="IS100"
gene complement(54689..55471 /locus-tag="y0042"
)
)
CDS complement(54689..55471 /locus-tag="y0042"
)
)
/function="IS and transposon
related functions"
/note="IS100; orfB; residues 1 to
260 of 260 are 100.00 pct
identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83637.1"
/db-xref="GI:21956701"
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SLISAAPALSQQAVDQEWESYMDFL
EHLLEHEKLARHQKQAMYTRMAAFPAVKTFEEY
DFTFATGAPQKQLQSLRSLSFIER
NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF
TTAADLLQLSTAQRGRYKTLQ
RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAKR
YEKSAMILTSNLPFGQWDQTFAGD
AALTSAMLDRILHSHVVQIKGESYRLRQKRKAG
VIAEANPE"
gene complement(55468..56490 /locus-tag="y0043"
)
)
CDS complement(55468..56490 /locus-tag="y0043"
)
)
/function="IS and transposon
related functions"
/note="IS100; orfA; residues 1 to
340 of 340 are 100.00 pct
identical to residues 1 to 340 of
340 from GenPept : >gb|AAC13168.1|
(AF053947) putative transposase
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83638.1"
/db-xref="GI:21956702"
/translation="MVTFTVMEIKILHKQGMSS

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gene	56560..56985	/locus-tag="y0044"
CDS	56560..56985	/locus-tag="y0044" /function="IS and transposon related functions" /note="IS1541a; residues 6 to 141 of 141 are 100.00 pct identical to residues 17 to 152 of 152 from GenPept : >gb AAL27370.1 AF426171-1 (AF426171) transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83639.1" /db-xref="GI:21956703" /translation="MHRSLHIVFAPKYRRQVFYR EKRAIGSILRKLCEWKNVNIIEA EYCVDDIHMLLEIPPKMSVSGFMGYLKGKSSLML YEQFGDLKFYKRNREFWCRGGYVD TVGKNTARIQEYIKHQLEEDKMGEQLSIPYPGSP FTGRK" /note="insertion element; partial" /insertion-seq="IS1541a" /locus-tag="y0045"
repeat-region	56575..57091	
gene	complement(57193..57432 )	/locus-tag="y0045"
CDS	complement(57193..57432 )	/locus-tag="y0045" /note="residues 1 to 79 of 79 are 75.94 pct identical to residues 3 to 81 of 81 from E. coli K12 : B3928; residues 1 to 79 of 79 are 77.21 pct identical to residues 1 to 79 of 79 from GenPept : >gb AAL22928.1  (AE008891) putative cytoplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83640.1" /db-xref="GI:21956704" /translation="MSFEVFEKLEVKVQQAIDTI TLLQMEIEELKEKNNTLTQEVQDA AGSREALVRENEQLKQEQHWQDRLRALLGKMEE V" /gene="glpF" /locus-tag="y0046" /gene="glpF" /locus-tag="y0046" /function="transport; transport of
gene	58060..58908	
CDS	58060..58908	

gene 59085..60608  
CDS 59085..60608

small molecules; carbohydrates,  
organic acids, alcohols"  
/note="residues 1 to 282 of 282  
are 82.62 pct identical to  
residues 1 to 279 of 281 from E.  
coli K12 : B3927; residues 1 to  
282 of 282 are 82.62 pct identical  
to residues 1 to 279 of 281 from  
GenPept :  
>gb|AAG59120.1|AE005623-11  
(AE005623) facilitated diffusion  
of glycerol [Escherichia coli  
O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
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uptake"  
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/db-xref="GI:21956706"  
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EISIIWGLGVAMAIYLTAAISGAHLNPAVTIALW  
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AALVYGLYSLFVDFEQTHQMVRGSTESQLAGI  
FSTYPNPHISVVQAFVLVETVITAI  
LMCLILALIDDDGNGIPRGPLAPLLIGILIAVIGA  
SMGPLTGFALNFARDLGPKAFSYL  
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YRALIGRHLPCDVCCTLEDEESTTI TTERKA"  
/gene="glpK"  
/locus-tag="y0047"  
/gene="glpK"  
/locus-tag="y0047"  
/function="enzyme; central  
intermediary metabolism: Pool,  
multipurpose conversions"  
/note="residues 7 to 507 of 507  
are 84.63 pct identical to  
residues 2 to 502 of 502 from E.  
coli K12 : B3926; residues 5 to  
507 of 507 are 84.49 pct identical  
to residues 7 to 509 of 509 from  
GenPept :  
>gb|AAG59119.1|AE005623-10  
(AE005623) glycerol kinase  
[Escherichia coli O157:H7 EDL933]"  
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/transl-table=11  
/product="glycerol kinase"  
/protein-id="AAM83642.1"  
/db-xref="GI:21956707"  
/translation="MTTENTTQKKYIVALDQGT  
SSRAVLDHNNANIVVSQREFTQI  
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EIAGIGITNQRETTIVWDKVTGKP  
VYNAIVWQCRRTADICEKLLKKEGLEEYIRHNTGL  
VVDPYFSGTKVKWILDNVEGARER  
AERGELLFGTVDTWLVNMTQGRVHVTDYTNASR  
TMMFNIRTKEDDRMLKALNIPRA  
MLPEVPSSEIYKGTNIGGGGTRIPAGIAGDQ  
QAALFGQLCVQPGMAKNITYGTGCF  
LLMNTGEEAVQSTHGLLTTIACGPRGEVNYALEG

		AVFIGGASIQWLRDELKLGIDATD SEYFATKVKNSNGVYVPAFTGLGAPYWDPYARG AIFGLTRGVNSNHIIIRATLESIA QTRDVLDAQADSGARKLSLRVDGGAVANNFLMQ FQADILGTRVERPAIRESTALGAA FLAGLAGTGFWDLLDEVKSKASIEREFRPGIETTE RDIRYKGWKKAVARARDWEEHDE"
gene	60737..61855	/gene="glpX" /locus-tag="y0048"
CDS	60737..61855	/gene="glpX" /locus-tag="y0048" /function="phenotype; Not classified" /note="unknown function in glycerol metabolism; residues 37 to 372 of 372 are 84.22 pct identical to residues 1 to 336 of 336 from E. coli K12 : B3925; residues 37 to 372 of 372 are 84.22 pct identical to residues 1 to 336 of 336 from GenPept : >dbj BAA09535.1  (D55718) GlpX [Klebsiella aerogenes]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83643.1" /db-xref="GI:21956708" /translation="MRVKRVQLTPLRLQVRKVIE FLPIFSFSIPQSTGLTMKRELAIE FSRVTEAAALAGYKWLGRGDKNAADGAAVQAMRI MLNQVNIDGRIVIGEGIDEAPML FIGEHVGTGGQDAVDIAVDPIEGTRMTAMGQANA LAVLAVGDQGTFLHAPDMYMEKLV VGPAAKGAIDLNLPLEQNLCNIATALNKPLADLT VITLAKPRHDGIIAAMQQLGVKVF AIPDGDVAASILTCMPESEVDVVMYCIGGAPEGVI SAAVIRALDGDMDQGRLLPRHQVKG DSEDNRRIGEQLLRCKSMGIEAGNVQLQGDMA NDNVIFSATGKITGDLLEGIYRKG NMATTETLLIRGKSRTIRRRIRSHFLDRKDPALH EFLL"
gene	62010..62756	/gene="fpr" /locus-tag="y0049"
CDS	62010..62756	/gene="fpr" /locus-tag="y0049" /function="enzyme; central intermediary metabolism: Pool, multipurpose conversions" /note="residues 1 to 248 of 248 are 74.19 pct identical to residues 1 to 248 of 248 from E. coli K12 : B3924; residues 1 to 248 of 248 are 77.01 pct identical to residues 1 to 248 of 248 from GenPept : >gb AAL22924.1  (AE008890) ferredoxin-NADP reductase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="ferredoxin-NADP

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reductase"
/protein-id="AAM83644.1"
/db-xref="GI:21956709"
/translation="MAEWSGKITHIEHWTDALF
SLQVNAPVDPFTAGQFAKLALDIN
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IPDCDTLWMLATGTAIGPYLSILQEGQDLERFKH
LVLVHAARFAHDL SYLPLMQOLEQ
RYNGKLRIQT VVSREESPGSLTGRVPALIENGAL
EAAVGLKIDAKDSHVMLCGNPGMV
RDTQQLLKQREMRKHLRRKPGHMTSEQYW"
gene      complement(63097..63597 /locus-tag="y0050"
)
CDS       complement(63097..63597 /locus-tag="y0050"
)

/notes="residues 23 to 163 of 166
are 66.66 pct identical to
residues 1 to 141 of 146 from E.
coli K12 : B3921"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83645.1"
/db-xref="GI:21956710"
/translation="MVSCDLEVHFAEIMLGKWIC
SSMTIQWCFSFKGRIGRREFWIW
MGLWLLAMLVIFTLAGKEWLP IQSASFALVFLW
PTAAVVVKRLHDRNKAGWAWALLAV
LAWMLMAGNWQMLTPIWQWGVGRFIPTLIFVMMF
IDCGAFLGT EGDNRFGPEAVPVKF FADKAK"
/locus-tag="y0051"
/locus-tag="y0051"
/notes="residues 11 to 204 of 204
are 56.18 pct identical to
residues 10 to 193 of 199 from E.
coli K12 : B3920; residues 10 to
203 of 204 are 57.21 pct identical
to residues 7 to 192 of 198 from
GenPept : >gb|AAL22922.1|
(AE008890) putative periplasmic
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83646.1"
/db-xref="GI:21956711"
/translation="MRIILLALLLITFMLITT
INHAHADPTNDSSPPEKAGPIAP
YLLFNAPTFDLTLVKFRESYNRANPTLPINEFHA
ITVKEDSPPLTRAASKINENLYAS
TALEKGTGKIKTLQITYLPKGN EKTAKLLAIN
YMAALMRQFEPTLSVVQSLANVQK
LLETGKGS PFYAHTIGAIRYVVDNGEKGLTFAV
EPIKLSLSEA"
/locus-tag="tpiA"
/locus-tag="y0052"
/locus-tag="tpiA"
/locus-tag="y0052"
/function="enzyme; energy
metabolism, carbon: Glycolysis"

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/note="residues 1 to 255 of 255  
 are 82.35 pct identical to  
 residues 1 to 255 of 255 from E.  
 coli K12 : B3919; residues 1 to  
 255 of 255 are 84.70 pct identical  
 to residues 1 to 255 of 255 from  
 GenPept : >gb|AAD16183.1|  
 (AF098509) triose phosphate  
 isomerase [Enterobacter cloacae]"  
 /codon-start=1  
 /transl-table=11  
 /product="triosephosphate  
 isomerase"  
 /protein-id="AAM83647.1"  
 /db-xref="GI:21956712"  
 /translation="MRHPLVMGNWKLNGSTHMVN  
 ELIAGLRKELSTVDGCGVAIAPPA  
 IYLNQAKHELAGSRIALGAQNVVDVNLGSAFTGET  
 SAEMLKDIGAQYIIIGHSEERRYH  
 QESDELIAKKFGVLKEIGLIPVLCIGESEAEAEA  
 GQTEAVCAKQLDAVLNLTGLVKAFE  
 GAVIAYEPIWAIGTGKSATPAQAQAVHKFIRDHI  
 AKQDAAVAAQVVIQYGGSVNDKNA  
 AELFTQFPDIDGALVGGASLKADAFVIVKAAAKA  
 KKA"

gene complement(65442..66737 /locus-tag="y0053"  
 )

CDS complement(65442..66737 /locus-tag="y0053"  
 )

/function="regulator"  
 /note="residues 28 to 405 of 431  
 are 30.26 pct identical to  
 residues 4 to 358 of 383 from  
 GenPept : >emb|CAB87565.1|  
 (AJ277295) FldY protein  
 [Sphingomonas sp. LB126]"  
 /codon-start=1  
 /transl-table=11  
 /product="putative transcriptional  
 regulator"  
 /protein-id="AAM83648.1"  
 /db-xref="GI:21956713"  
 /translation="MPKRQVLFKLKLNKITRRN  
 MQKKNDNRNSIKIMQIRAFCMIAEQ  
 GAASLAALNLFRTQSAITRSIRDLEHTLAISLFE  
 RHAKGMLLTDLGNVILPRARSAME  
 ELTRIPALLRRLLQQRDDEGIEDLEPTWLFNERRL  
 QIFLSLYRQQHALHVAQALDITQS  
 AVSAALKVLEKGAGMYLFRHTPKGMPLTPAGHEI  
 APCISRALNALHHIPEEITAHRGD  
 LTGSVRVGALPLSRARLLPQAMIKLISRHPGIKI  
 VTNSEGFTALIAELRAGDIDIFIIG  
 ALRNEKMLLDIHSEILFEEELILLARPNNHPLSDR  
 RVKNQELKDIQWVLPFNHAPSRHL  
 LEVAFCKMGLASPQPVVSEGDPAVVRALLGSDM  
 VAAVSSHQLDFEVSEGILIPLVN  
 LTGTRREIGLMTRQKALNSPATDALINCVREVIQ  
 SSNDK"

gene 66730..67551 /locus-tag="y0054"  
 CDS 66730..67551 /locus-tag="y0054"

/note="residues 34 to 272 of 273  
 are 65.41 pct identical to

gene 67548..68261  
CDS 67548..68261

residues 3 to 238 of 244 from  
GenPept : >emb|CAC46343.1|  
(AL591788) conserved hypothetical  
protein [Sinorhizobium meliloti]"  
/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83649.1"  
/db-xref="GI:21956714"  
/translation="MGNKTHYFPLIKPCQNPRQL  
KQQKKEKDMAMIPQKTALVVSAAHS  
ADFWRRAGGAIALHVEQGYQVHVIVCLSYGERGES  
AKLWRKGDMTEERVKASRHTEAQA  
AANVLGASIEFFDMGDYPLRADKESLFRADVFR  
RIQPHFVLTHSLADPYNVDHPLAA  
NLAQEARIIAQAEGYRPGEAIIAGPPVVCYCFEPHQ  
PEQCGWKPDVLLDITSVWEKKYAA  
IQCMAGQEHLWEYYTRVALQRGVQAKRNIGIAST  
KTIHGEQYQSLFPRVTEDLS"  
/locus-tag="y0055"  
/locus-tag="y0055"  
/note="residues 6 to 229 of 237  
are 61.60 pct identical to  
residues 1 to 224 of 224 from  
GenPept : >emb|CAB87566.1|  
(AJ277295) FldZ protein  
[Sphingomonas sp. LB126]"  
/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83650.1"  
/db-xref="GI:21956715"  
/translation="MSLVNMKGVVVNIERIAELA  
LLQRFAYEGVATVHEAQLRQGLD  
ERIKPIQQGRCIAGNAVTVLTPGDNWFMFHAVVE  
QCQPGDVLLVAPTSECHDGFFGDL  
LATSLLARGVVALVGDIGIRDSQTLREMNFVWS  
RAVWAQGTVKASLGSVNVVVICAG  
QLVNPGDIVVADDDGVVIVPREQATAIADAAQTR  
VDLETSKRQRLANGELGLDIYQMR  
APLAKKGLRYVNSLNALKS"  
/locus-tag="y0056"  
/locus-tag="y0056"  
/note="residues 2 to 471 of 475  
are 52.20 pct identical to  
residues 3 to 471 of 477 from E.  
coli K12 : B0770; residues 2 to  
471 of 475 are 52.20 pct identical  
to residues 3 to 471 of 477 from  
GenPept :  
>gb|AAG55099.1|AE005254-11  
(AE005254) putative membrane pump  
protein [Escherichia coli O157:H7  
EDL933]"  
/codon-start=1  
/transl-table=11  
/product="putative membrane pump  
protein"  
/protein-id="AAM83651.1"  
/db-xref="GI:21956716"  
/translation="MKNKIWKLCILVMIPLVIWF  
IPPEGLTELSWRLSGFYLAACIG

gene 68327..69754  
CDS 68327..69754

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LILKPFSEAVVLLGVVGFAGFFLNNTSQILVGYA
TSTVWLVFAAFGISISFVKTLGLR
RIAFHMRIRFCGSTTLRLGYVTAFLFVISPVTSP
NTARSGGIVFPIILSVVKALGSEP
GDTAKKAGSYLMSNIYFVMKVSSFMITAMAPNL
LAADFAAKILGIHLDWGVWALAMV
VPGLLLLLIIPAVGYIYLDKPELKKVDNKKIADEG
LAELGPITRNEKLLVGIFISALLG
WALPSLLGQLEGITLKDITAVAIMAMALCILLG
VIKWDVQLNKGAWNTLLWFGGII
GLASALSKEKVFDLANLIQNNVDFGHNPFIALT
IIGFLSIIIRYFFASASSYAIAML
PVFLTGVKGAGADPMALALVLAATNSYGGALTHY
GGGSAPIIFGAGYNNVQWQWASGA
VIATVCFIVMTIVGYVWQQLGFVK"
gene      69830..70648      /gene="modA"
CDS       69830..70648      /locus-tag="y0057"
                                /gene="modA"
                                /locus-tag="y0057"
                                /function="putative transport;
                                transport of small molecules;
                                Other"
                                /note="residues 48 to 271 of 272
                                are 55.55 pct identical to
                                residues 5 to 229 of 230 from
                                GenPept : >dbj|BAB21454.2|
                                (AB050935) ProX protein
                                [Pseudomonas straminea]"
                                /codon-start=1
                                /transl-table=11
                                /product="molybdate-binding
                                periplasmic protein precursor"
                                /protein-id="AAM83652.1"
                                /db-xref="GI:21956718"
                                /translation="MACLLAQYNSGDILMKYSNV
                                IVSGLCMSMVSLATAAPTEVPSDE
                                PVTLRIISSMATRQFLTEVIAQFAQQSKYQVELE
                                SVGGVDATKRVEAGEAFDVVILSA
                                NAIDKLIDSGKILPNSRIDLVKSGVAIAVKEGAQ
                                IMDVSSEETVKQAVLAANTIAYST
                                GPSGVYLTEVFEHWGIAEQIKDRIVKVPVPGVPVG
                                SLVAKGEVELGLQLSELLHLKGI
                                IILGPLPTDIQIMTHFSAGVPLKTNQQKAIKVLL
                                DFLASPAATEAKIKNGMEPI"
gene      complement(70898..71920) /gene="sbp"
                                /locus-tag="y0058"
CDS       complement(70898..71920) /gene="sbp"
                                /locus-tag="y0058"
                                /function="transport; transport of
                                small molecules; anions"
                                /note="residues 12 to 340 of 340
                                are 83.58 pct identical to
                                residues 1 to 329 of 329 from E.
                                coli K12 : B3917"
                                /codon-start=1
                                /transl-table=11
                                /product="periplasmic
                                sulfate-binding protein of
                                sulfate/thiosulfate ABC
                                transporter"

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/protein-id="AAM83653.1"
/db-xref="GI:21956719"
/translation="MITIIFLRSGSMRKWGVGLS
LLVLASGAMAKDIQLLNVSYPTR
EFYQEYNQAFSKYWQQQTGDKVTVRQSHGSGKQ
ATSVINGIEADVLTILAYVDVAI
AERGRIDKNWIKRLPDNSAPYTTIVFLVRKGNP
KQIHDWSDLVKPGTSVITPNPKTS
GGARWNYLAAWGYALEHNNNDQAKAQEFVNALYK
NVEVLDSGARGATNTFVERGIGDV
LIAMENEALLAVNEVNGNQFDIVTPSVSILAEP
VSVDKVVDKRGTRDVADAYLKYL
YSPGQTIAAKNYYRPRDPVVAAKFAKEFPQLKL
FTIDEVFGGWTQAKKTHFATGGVF DEISKR"
gene      complement(72108..73091 /gene="pfkA"
)
CDS       complement(72108..73091 /locus-tag="y0059"
)
          /gene="pfkA"
          /locus-tag="y0059"
          /function="enzyme; energy
          metabolism, carbon: Glycolysis"
          /note="residues 1 to 327 of 327
          are 77.06 pct identical to
          residues 1 to 320 of 320 from E.
          coli K12 : B3916; residues 1 to
          327 of 327 are 79.20 pct identical
          to residues 1 to 320 of 320 from
          GenPept : >gb|AAD16179.1|
          (AF098509) phosphofructokinase
          [Enterobacter cloacae]"
          /codon-start=1
          /transl-table=11
          /product="6-phosphofructokinase I"
          /protein-id="AAM83654.1"
          /db-xref="GI:21956720"
          /translation="MVKKIGVLTSGGDAPGMNAA
          IRGVVRAALSAGLDVFGIEDGYLG
          LYENRMKKLDRYSVSDMINRGGTFLGSRFFEFR
          DPEVRKVALKNMHERGIDGLVVIG
          GDGSYAGADLLTKEGGIHCVGLPGTIDNDVAGTD
          YTIGFFTALETVVEAIDRLRDTSS
          SHQRISIVEVMGRYCGDLTLAAAIAGGCEFIAIP
          EVEFKRDDLVAEIKAGIAKGGKHA
          IVAITEKLDDISLAKYIEKTEGRETRGTVLGH
          IQRGGAPVAYDRILASRMGAYVDL
          LLQDHDYKKGGFCEVGVQNEKMHVILISVCIAPEN
          KSKFKEDWYDTAKKLF"
gene      complement(73309..74211 /locus-tag="y0060"
)
CDS       complement(73309..74211 /locus-tag="y0060"
)
          /function="putative transport"
          /note="residues 1 to 293 of 300
          are 78.49 pct identical to
          residues 1 to 293 of 300 from E.
          coli K12 : B3915; residues 1 to
          293 of 300 are 79.86 pct identical
          to residues 1 to 293 of 300 from
          GenPept : >gb|AAL22901.1|
          (AE008889) putative CDF family
          transport protein [Salmonella

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typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="putative efflux permease
protein"
/protein-id="AAM83655.1"
/db-xref="GI:21956721"
/translation="MDPQYARWVKAALSATALA
SILLIIKIFAWWHTGSVSLAALV
DSLVDLAASLTNLFVVRYSLQPADEHTFGHGKA
ESLAALAQSMFISGSALFLFLTGF
RHLASPEPLQDPSIGIGVTILVALFSTLILVTFQR
WVVRKTHSQAIRADMLHYQSDVLM
NGAILIALALSWYGERRADALFALGIGVYILYSA
LRMGYEAQVSLDRALPDDERQOI
IDIVTSWPGVIGAHDLRTRRSQTFRFIQLHLEME
DMMPLMEAHVLAEQVEHALLYRFP
GADVLIHQDPCSVVFKERHAHWEL"
/locus-tag="y0061"
/locus-tag="y0061"
/function="IS and transposon
related functions"
/note="unidentified IS; residues 2
to 37 of 40 are 47.22 pct
identical to residues 89 to 124 of
253 from GenPept :
>emb|CAC35348.1| (AJ277063)
putative transposase [Vibrio
salmonicida]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83656.1"
/db-xref="GI:21956722"
/translation="MIFIDNNIIRTHQHGTVAVS
ESDESIIKHRGVTRQKLISR"
/locus-tag="y0062"

gene      complement(74773..75732
)
CDS       complement(74773..75732 /locus-tag="y0062"
)

/note="residues 15 to 314 of 319
are 56.00 pct identical to
residues 4 to 287 of 292 from E.
coli K12 : B3411; residues 16 to
319 of 319 are 62.01 pct identical
to residues 6 to 313 of 313 from
GenPept : >gb|AAL23539.1|
(AE006471) putative cytoplasmic
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83657.1"
/db-xref="GI:21956723"
/translation="MIAQEDAHDYHRPMKTTPTP
HDALFKNFMTQPATACDLLEFHLF
PELRQLCDLSTLRLESGSFIENNLACYSVDVLYS
LKTTVGDGYVYALIEHQSSPDKHM
AFRLMRYAIAAQSHLEAGYDKLPLVIPILFYHG
MVTPTYPPYMSWLHAFNQPELAGQL
YCGNPLVDVTVIPDHEIMTHRRIALLELLQKHI

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RQRDLSELLDQLVILIASGYTTD
QLKSAINYIIQVGETAEPEVFIIRSLAHLRPEHEE
SLMTIAQKLEQKGEARGIVKGRVE
GRVEGAQETALKIARTMLANGLDRATVMKMTGLS
EEELTQIHH"
gene      complement(75777..75953 /locus-tag="y0063"
)
CDS       complement(75777..75953 /locus-tag="y0063"
)
                                           /codon-start=1
                                           /transl-table=11
                                           /product="hypothetical"
                                           /protein-id="AAM83658.1"
                                           /db-xref="GI:21956724"
                                           /translation="MPSLLASTLQISPLYECINV
LTDVATTINNQETDIQQLVACKHYR
VALMRTHAAPKSPQ"
gene      75932..76039 /locus-tag="y0064"
CDS       75932..76039 /locus-tag="y0064"
                                           /note="residues 1 to 33 of 35 are
51.51 pct identical to residues
230 to 262 of 326 from GenPept :
>emb|CAB54522.1| (AJ245959) Int
protein [Bacteriophage WPhi]"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="hypothetical"
                                           /protein-id="AAM83659.1"
                                           /db-xref="GI:21956725"
                                           /translation="MKQEVKANASGKLFNMDYKG
FGETQRNVKPDLPFG"
gene      76049..76252 /locus-tag="y0065"
CDS       76049..76252 /locus-tag="y0065"
                                           /note="residues 1 to 56 of 67 are
80.35 pct identical to residues
269 to 324 of 326 from GenPept :
>emb|CAB54522.1| (AJ245959) Int
protein [Bacteriophage WPhi]"
                                           /codon-start=1
                                           /transl-table=11
                                           /product="hypothetical"
                                           /protein-id="AAM83660.1"
                                           /db-xref="GI:21956726"
                                           /translation="MLRHTCASHFMMNSRNIIAL
QQILRHANIQPTMAYAHLPDYLQ
NTVILTPLKGGGLAAETRPQSVHT"
gene      complement(76410..76898 /locus-tag="y0066"
)
CDS       complement(76410..76898 /locus-tag="y0066"
)
                                           /note="residues 51 to 162 of 162
are 62.50 pct identical to
residues 1 to 112 of 122 from E.
coli K12 : B3914; residues 1 to
162 of 162 are 52.46 pct identical
to residues 1 to 156 of 166 from
GenPept : >gb|AAL22900.1|
(AE008889) periplasmic repressor
of cpx regulon by interaction with
CpxA, rescue from transitory
stresses [Salmonella typhimurium
LT2]"

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		<pre> /codon-start=1 /transl-table=11 /product="putative solute-binding periplasmic protein of ABC transporter" /protein-id="AAM83661.1" /db-xref="GI:21956727" /translation="MRKVTTLVMSMFVLGSSAA FAADNTKVTGYHGDGKMMNNKKG DRGHHNMF DGINLTEQQRQMRDLMRQSHSQPR LDLEDREAMHKLITADKFDEAAVR AQAQKMSQNKIERHVEMAKVRNQMYNLLTPEQKE ALNKKHQERIEKLQOKPAAQPSSA QK" </pre>
gene	77048..77770	<pre> /gene="cpxR" /locus-tag="y0067" </pre>
CDS	77048..77770	<pre> /gene="cpxR" /locus-tag="y0067" /function="putative regulator" /notes="residues 9 to 238 of 240 are 90.43 pct identical to residues 1 to 230 of 232 from E. coli K12 : B3912" /codon-start=1 /transl-table=11 /product="transcriptional regulator in 2-component system" /protein-id="AAM83662.1" /db-xref="GI:21956728" /translation="MRQGEITMHKILLVDDRE LTSLLKELLEMEGFNVVVAYDGEQ ALSQDSSIDL LLDIMMPKNGIETLKL RQH QTPVIMLTARGSELDRVLGLELGA DDYLAKFPNDRELVARIRAILRRSNWSEQQNAE QGAPTLVDCLQNFGRQEASFEG QPLELTGTEFTLLYLLAQHLGQVVSREHLSQEV GKRLTPFDRAIDMHISNLRKLPD RKDGLPWFKTLRGRGYLMVSET" </pre>
gene	77767..79143	<pre> /gene="cpxA" /locus-tag="y0069" </pre>
CDS	77767..79143	<pre> /gene="cpxA" /locus-tag="y0069" /function="putative regulator; global regulatory functions" /notes="acting on arcA; residues 1 to 454 of 458 are 80.83 pct identical to residues 1 to 454 of 457 from E. coli K12 : B3911" /codon-start=1 /transl-table=11 /product="probable sensor protein, histidine protein kinase" /protein-id="AAM83663.1" /db-xref="GI:21956729" /translation="MINSLTTRIFAIWF TLA LVLVLMVPKLD SRQLTVLLDSEQR QGTMLQHI EAE LANDPANDL MWRRLHRAIEK W APPQHLLIVTSEGRIGVQRQEV QMVRNFIGQSDNADQPKKKYGRVEMVGPFSIRD GEDNYQLYLIRPANSQSDFINLM FDRPLLLL IATMLISAPLLLWLAWSLAKPARKL NAADDVARGNLKHPELES GPQEF LATGASFNQMISSLDRMVVAQQLRISDISHELRT </pre>

```

PLTRLQLATALMRRRHGEGKELER
IEMEAQRLDSMINDLLVLSRSQHKNELHREPIKA
DELWSDVLENAQFEAEQMGKTLVV
TAPPGPWPLFCNPAALDSALENIVRNALRYSHHH
IAVAFSIDNQGVTTIIVDDDGPGVS
PEDREQIFRPFYRTDEARDRASGGTGLGLAIVET
AVSQHRGWVKAEDSPLGGLRLIVW LPLHPLKS"

gene      complement(78938..79090 /locus-tag="y0068"
)
CDS       complement(78938..79090 /locus-tag="y0068"
)
          /codon-start=1
          /transl-table=11
          /product="hypothetical"
          /protein-id="AAM83664.1"
          /db-xref="GI:21956730"
          /translation="MGYLRLLPTLDADSPRFQQL
          GGPILFLPTPDGLGLHYDKMAGIF VHGPLG"

gene      complement(79192..80256
)
          /locus-tag="y0070"

CDS       complement(79192..80256 /gene="ada"
)
          /locus-tag="y0070"
          /function="enzyme; DNA -
          replication, repair,
          restriction/modification"
          /note="residues 6 to 350 of 354
          are 52.75 pct identical to
          residues 10 to 353 of 354 from E.
          coli K12 : B2213; residues 6 to
          345 of 354 are 65.58 pct identical
          to residues 18 to 357 of 360 from
          GenPept : >emb|CAD16277.1|
          (AL646070) probable ADA regulatory
          of adaptative response contains:
          methylated-DNA--protein-cysteine
          methyltransferase EC 2.1.1.63
          O-6-methylguanine-DNA
          transcription regulator[Ralstonia
          solanacearum]"
          /codon-start=1
          /transl-table=11
          /product="O6-methylguanine-DNA
          methyltransferase; transcription
          activator/repressor"
          /protein-id="AAM83665.1"
          /db-xref="GI:21956731"
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          GQFVYAVKTTGIYCRPSCPSRRAK
          AENIEFFIDNTAAEQAGYRCKRCQPTQLSRAQQ
          QVEKISQACRLIELAETPPKLNEL
          AAQLGLSTFYFHRLFKAITGLTPKGYANATRSER
          IRAQLSHGGSVTDAlFEAGYNSSS
          RFYAQSQQLLGMTPTIRYRKGCCDARLHFAVGESS
          LGAILVAKSELGVCAILLGDDPVR
          LVQQLQDKFPQANLVGGDAEFQWVAQVVGCVQA
          PKLGLNPLDIRGTAFOQRVWQAL
          REIPIGETASYADIASRIGSPTAVRAVAGACAAAN
          ILAVAPCHRVIRQDGLSGYRWG
          VERKRLLLEREGVEKEAEDH"

gene      80349..80933 /locus-tag="y0071"

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CDS	80349..80933	/locus-tag="y0071" /note="residues 33 to 194 of 194 are 80.24 pct identical to residues 1 to 157 of 157 from E. coli K12 : B3606" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83666.1" /db-xref="GI:21956733" /translation="MLLNFCFTPLPPLATAALNKG FNYAPALIIGGHMLNIVLFEPEIP PNTGNIIRLCANTGCQLHLIKPLGFTWDDKRLRR AGLDYHEFADIKHHHDYQAFLDSE KLDSTQPARLFALTTKGTPAHSAVSQYANDYLLF GPETRGLPAYILDALPAQQKIRIP MQADRSRSMNLSNAVSVVVVEAWRQLGYPALLKE "
gene	complement(81056..81880)	/gene="cysE"
CDS	complement(81056..81880)	/locus-tag="y0072" /gene="cysE"  /locus-tag="y0072" /function="enzyme; amino acid biosynthesis: Cysteine" /note="residues 2 to 274 of 274 are 86.08 pct identical to residues 1 to 273 of 273 from E. coli K12 : B3607" /codon-start=1 /transl-table=11 /product="serine acetyltransferase" /protein-id="AAM83667.1" /db-xref="GI:21956734" /translation="MMSSEELQVNSNIKSEARA LAECEPMLASFHFHATLLKHENLGS ALSYLANKLANPIMPATIAIREVVEEAYRSDAHM IVSAARDILAVLRDPDAVDKYSTP LLYLKGFFHALQAYRIGHNLWAQDKRALAIYLQNQ VSVAFGVDIHPAATIGCGIMLDHA TGVIGETAVVENDVSIQSVTLGGTGKTSGRDRH PKIREGVMIGAGAKILGNIEVGRG AKIGAGSVVLQSVPAHTTAAGVPARIVGKPESDK PSLMDMQHFNGSIQGFYGDGI"
gene	complement(82143..83162)	/gene="gpsA"
CDS	complement(82143..83162)	/locus-tag="y0073" /gene="gpsA"  /locus-tag="y0073" /function="enzyme; energy metabolism, carbon: Aerobic respiration" /note="residues 1 to 336 of 339 are 84.52 pct identical to residues 1 to 336 of 339 from E. coli K12 : B3608" /codon-start=1 /transl-table=11 /product="glycerol-3-phosphate

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dehydrogenase (NAD+) "
/protein-id="AAM83668.1"
/db-xref="GI:21956735"
/translation="MNTNPASMAVIGAGSYGTAL
AITLARNGHQVVLWGHDPKHIIQL
QQDRCNRAFLPDAAFPDTRLRLTDLACALAAASRD
VLVVVPSHVFGAVLHQLKPHLRKD
ARIVWATKGLEAETGRLLQDVAREVLGEAIPLAV
ISGPTFAKELAAGLFTAIALASTD
VQFSEDLQQLLHCGKSFVRVSNPDFIGVQLGGAV
KNVIAIGAGMSDGIGFGANARTAL
ITRGLAEMTRLGTALGADPSTFMGMAGLGDLVLT
CTDNQSRNRRFGIMLQGGLGVKEA
QDNIGQVVVEGYRNTKEVLALAQRHGVEMPIEQI
YQVLYCHKNAREAALTLLGRTKKD EKIGI"
gene      complement(83162..83638) /gene="secB"
)
CDS       complement(83162..83638) /locus-tag="y0074"
) /gene="secB"

/locus-tag="y0074"
/function="transport; protein,
peptide secretion"
/note="may bind to signal
sequence; residues 1 to 158 of 158
are 91.13 pct identical to
residues 1 to 155 of 155 from E.
coli K12 : B3609"
/codon-start=1
/transl-table=11
/product="protein export;
molecular chaperone"
/protein-id="AAM83669.1"
/db-xref="GI:21956736"
/translation="MSEQNNTIEMAFQIQRIYTKD
ISFEAPNAPQVFQQDWQFEVKLDL
DTASSQLAEDVYEVVLRVTVTASLGEETAFLCEV
QQGGIFSVAGIEGTQLAHCLGAYC
FNILFFPYARECITSLVSRGTFPQLNLAPVNFDA
FMNLYLQQQAEGEVEGVEQRQDA"
gene      complement(83726..83974) /gene="grxC"
)
CDS       complement(83726..83974) /locus-tag="y0075"
) /gene="grxC"

/locus-tag="y0075"
/function="enzyme; biosynthesis of
cofactors, carriers: Thioredoxin,
glutaredoxin, glutathione"
/note="residues 1 to 82 of 82 are
78.04 pct identical to residues 1
to 82 of 83 from E. coli K12 :
B3610; residues 1 to 82 of 82 are
85.36 pct identical to residues 1
to 82 of 83 from GenPept :
>gb|AAL22561.1| (AE008872)
glutaredoxin 3 [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="glutaredoxin 3"
/protein-id="AAM83670.1"

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/db-xref="GI:21956737"
/translation="MAKIEMYTKATCPFCHRAKA
LLNAKGAAFHEIAIDNDPAKREEM
IARSGRTTVPQIFIDGQHIGGCCDDLHALDARGGL
DPLL"
gene      complement(84093..84527 /locus-tag="y0076"
)
CDS       complement(84093..84527 /locus-tag="y0076"
)

/note="residues 2 to 144 of 144
are 65.73 pct identical to
residues 1 to 143 of 143 from E.
coli K12 : B3611; residues 2 to
144 of 144 are 67.83 pct identical
to residues 1 to 143 of 143 from
GenPept : >gb|AAL22562.1|
(AE008872) putative
Rhodanese-related
sulfurtransferases [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83671.1"
/db-xref="GI:21956738"
/translation="MLQEI MQFISQHPILSLAWV
LLFGAVVFTSFKNLSLKVKEVTRG
EATRLINKEDAVVVDIRREDYRKGHIANSLNI
PSDIKGNLGELEKHKKTQPIIVVC
AMGTTSRASADMLSKAGFERVFTLKEGISGWSGE
NLPLARGK"
/locus-tag="y0077"
/locus-tag="y0077"
/note="residues 1 to 515 of 515
are 83.30 pct identical to
residues 1 to 514 of 514 from E.
coli K12 : B3612; residues 1 to
515 of 515 are 83.88 pct identical
to residues 1 to 514 of 514 from
GenPept : >gb|AAL22563.1|
(AE008872) phosphoglyceromutase
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="putative
2,3-bisphosphoglycerate-independen
t phosphoglycerate mutase"
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EQQDNAILNAKTPVMDVLWQQQPH
TLIAASGLDVGLPDGQMCNSEVGHVNLGAGRIVY
QDLTRLDEIKEGDFFTNPTLTAA
VDNAVKTGKAVHIMGLLSAGGVHSHEDHIMAMVE
LAAKRGATAIYLAHFLDGRDTPPR
SAESSLKRF TAKFAELGNRIASIIIGRYAMDRD
NRWDRVQLAYDLLTQAKGEFTADN
AVAGLQAA YARGENDEFVKPTVIQATGEADAAMN
EGDTLIFMNFRA DRARQITRTFVN
AEFDGFKRDKV VNGDFIML TEYAADIKVACAYP
PASLTNTFGEWLMKHKDTQLRISE
TEKYAHVTTYFYNGGVEEPPFKGEDRILINSPKVAT

```

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YDLQPEMSSAELTEKLVSIGSGK
YDVIICNYPNGDMVGTGDYDAVKAVETLDNCI
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QMRDPATGQAHTAHTSLFVPLIYVGNKAVKAVEG
GKLSADIAPTMLSLMEMEIPQEMTG KPLFIVE"
/locus-tag="y0078"
/locus-tag="y0078"
/function="putative membrane"
/notes="residues 39 to 456 of 456
are 63.39 pct identical to
residues 24 to 427 of 427 from E.
coli K12 : B3613; residues 40 to
456 of 456 are 65.70 pct identical
to residues 25 to 427 of 427 from
GenPept : >gb|AAL22564.1|
(AE008872) paral putative membrane
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="AAM83673.1"
/db-xref="GI:21956740"
/translation="MKDRELLAKSITTKDAVSDG
RESPSLLSDKLSRLPWSILYASVF
CAGVLLLPFSGQAVEPPVAAKASENKNQLTKLQQ
DIAEKEKSVQQKKQRSSLLDQLK
QENTISQTSRSLRETOATLAELSKDIASLTISI
EKLQNQQSQQQSILSKQLAAAFKQ
GKHSSLLQLILSGEESQRSEIRLAYFSYLNEARQK
AIEELKQTRTTLIAEKKMLEQKON
QHKALLDEQKAQQQKLEQARIARQKTLTSLASL
EKDQQSLAELKLNESRLRDQIAKA
EREAKARAEREAKAARVREQVKVKEQQAKKTGS
SYKPSSESRSLMARTGGGRPGGQ
ALWVPVRGNVSHRFGEPLQGELRWKGMVITAPEGs
EVKAIADGRVLLADWLQGYGLVVV
IEHGKGDMSLYGYNQSALVNVGAQVKAGQPIALV
GTSGGQGEPSLYFEIRRQGGQAVNP QPWLGR"
/locus-tag="y0079"
/notes="disrupted by frameshift"
/pseudo
/locus-tag="y0080"
/function="enzyme; degradation of
small molecules; amino acids"
/notes="residues 1 to 341 of 341
are 92.08 pct identical to
residues 1 to 341 of 341 from E.
coli K12 : B3616"
/codon-start=1
/transl-table=11
/product="threonine dehydrogenase"
/protein-id="AAM83674.1"
/db-xref="GI:21956741"
/translation="MKALSCLKAEEGIWMTDVPQ
PELGHNDIMIKIRKTAICGTDVHI

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gene	86481..87851
CDS	86481..87851
gene	87875..88809
gene	complement(88947..89972)
CDS	complement(88947..89972)



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YNWDEWSQKTIPVPMVVGHEYVGEVVAIGQEVKG
FNIGDRVSGEGHITCGHCRNCRGG
RTHLCRNTVGVGVNRPGSFAEYLVIPAFNAFKIP
DNISDELAIAIFDPFGNAVHTLSF
DLVGEDVLVSGAGPIGIMAAVCKHVGARHVVIA
DVNRYRLDLARKMGVTRAVNVSK
NLNDVMTLGMTGEGFDVGLMSGAPAFRSLNS
MNHGGRIAMLGIPPSDMSIDWNQV
IFKGLFIKGIYGREMFETWYKMAALIQSGLDLTP
IITHRFPIDFQQGFDAMRSGKSG KVVLSWD"
gene      complement(89982..91223 /gene="kbl"
)
)
CDS      complement(89982..91223 /gene="kbl"
)
)
/locus-tag="y0081"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 20 to 413 of 413
are 84.77 pct identical to
residues 5 to 398 of 398 from E.
coli K12 : B3617"
/codon-start=1
/transl-table=11
/product="2-amino-3-ketobutyrate
CoA ligase (glycine
acetyltransferase)"
/protein-id="AAM83675.1"
/db-xref="GI:21956742"
/translation="MQLPILEITEMSLPCNKHPF
YQLEQQLDTRTEGLYKNERVIT
SAQQANIAVADGSRVINFCANNYGLANHPKLIA
AAKAGMDSHGFGMASVRFIGTQD
IHKELEHKLASFLGMEDAILYSSCFDANGGLFET
LLGPEDAIISDALNHASIIDGVRL
CKAKRYRYANNDMTELEAQLKQAKAEGARHIMIA
TDGVFSMDGVIANLKRVCDLADEY
QALVMVDDSHAVGVIGANGRGTHEYCEVMDRVDI
ITGTGLKALGGASGGYTAGRKELV
EWLRQSRPYLFSNSLAPAIVAASIEVLSLEEG
GALRDRLWANARLFREKMSAAGFT
LAGADHAIPVMLGEAKLAQDFANALLKEGIYVT
GFFFPVVPKQARIRTQMSAGHTT
EQVERAIEAFVRIGKQLNVIA"
gene      91394..92371 /gene="rfad"
)
)
CDS      91394..92371 /locus-tag="y0083"
)
)
/locus-tag="rfad"
/function="enzyme; surface
polysaccharides and antigens"
/note="residues 16 to 323 of 325
are 83.11 pct identical to
residues 1 to 308 of 310 from E.
coli K12 : B3619"
/codon-start=1
/transl-table=11
/product="ADP-L-glycero-D-mannohep
tose-6-epimerase"
/protein-id="AAM83676.1"
/db-xref="GI:21956744"
/translation="MCGCTQPRKLARVNTMIIVT

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gene 92016..92243  
CDS 92016..92243

gene 92390..93466  
CDS 92390..93466

GGAGFIGSNIVKALNNIGYKDILV  
VDNLKDGTKFVNLDLDIADYMDKEDFVASIVAG  
DDMGDIDAIFHEGACSSSTTEWDGK  
YMMDNQYQSKDILHFCILDRSIPFLYASSAATYQ  
GRTDNFIEDRQYEQPLNVYGYSKF  
LFDQYVREILPOADSQICGFRYFNVYGPREGHKQ  
SMASVAFHLNNQINAGERPKLFAG  
SENFKRDFIYVGDVADVNLFWFQNGVSGIFNCGT  
GRAESQAVADAVVDYHQSGPVEY  
IEFPEKLKGRYQAYTQADLTKLRAAGYGKPKFTV  
AEGVKEYLAWLNRSV"  
/locus-tag="y0082"  
/locus-tag="y0082"  
/note="residues 5 to 33 of 75 are  
48.27 pct identical to residues 94  
to 122 of 182 from GenPept :  
>dbj|BAAL1839.1| (D83187) delta  
9-fatty acid desaturase [Yarrowia  
lipolytica]"  
/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83677.1"  
/db-xref="GI:21956745"  
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MWVMLLTLCGSGKTAYPVFSTAV  
LAGQSLRLSLMQWIIITKVGQSNSTSSSLKN"  
/gene="rfaF"  
/locus-tag="y0084"  
/gene="rfaF"  
/locus-tag="y0084"  
/function="putative enzyme;  
macromolecule metabolism:  
Lipopolysaccharide"  
/note="lipopolysaccharide core  
biosynthesis; residues 5 to 351 of  
358 are 73.77 pct identical to  
residues 1 to 347 of 348 from E.  
coli K12 : B3620; residues 5 to  
351 of 358 are 78.38 pct identical  
to residues 1 to 347 of 348 from  
GenPept : >gb|AAL23754.1| (U52844)  
heptosyltransferase II WaaF  
[Serratia marcescens]"  
/codon-start=1  
/transl-table=11  
/product="ADP-heptose--lps  
heptosyltransferase II"  
/protein-id="AAM83678.1"  
/db-xref="GI:21956746"  
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SQSLYRTLKAEYPAADIDVMAPAW  
CRPLLARMEVRRHAIPMPLHGGAFAFEERRRLGL  
ALRETEYDRAYVLPNSFKSALIPY  
FSGIKRRIGWRGEMRYFLNLDRLRILDKQAFPMV  
QRYVALAYDKERIRSAADLPQPLL  
WPQLQVRDEEIAETTASFNLTDNRPIIGFCPGA  
FGPAKRWPYHYATLAQKLIDDGY  
QVILFGSAKDNEAGEDIRQALSDTDREYCLNLG  
QTSLEQAVVLIAACSAVVSNDGSL  
MHVAAALNKPLVALYGPSSPDFTPLSEKATVIR  
LITGYHKVRKGDSAQGYHQSLIDI

gene	93442..94431	QPEHVMAALEKQLATQEC SVKGGD" /gene="rfaC" /locus-tag="y0085" /gene="rfaC" /locus-tag="y0085" /function="enzyme; macromolecule metabolism: Lipopolysaccharide" /note="lipopolysaccharide core biosynthesis; residues 9 to 327 of 329 are 68.33 pct identical to residues 1 to 319 of 319 from E. coli K12 : B3621; residues 9 to 329 of 329 are 81.30 pct identical to residues 1 to 321 of 321 from GenPept : >gb AAL23755.1  (U52844) heptosyltransferase I WaaC [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="heptosyl transferase I" /protein-id="AAM83679.1" /db-xref="GI:21956747" /translation="MLSQRGLMHVLIVKTSSMG DVLHTLPALTDAMNAIPGIRFDWV VEEGFSQIPSWHPAVDKVIPVAIRWRKNWFGSD TRQERCDFKRVVQORSYDRVIDAQ GLIKSAALITRIAGTKKHGPDCKSAREPFASWFY NCRHEIDTKQHAVERIRQLFAKSL GYDKPESYGDYIAIQRFLNQLPADAGQYLVFLHA TTRDNKHWPESHVQVLIELVPTG LKIKLPWGAHEHQRALRLAEHFPHEVPLKLSL QQVAEVLGAKAVVSVDTLGSLT AALDRPNITLFGPTDPLGIGYGKQIAVISEQK KMDSLAPTIMARLETLS" /gene="kdtA" /locus-tag="y0086" /gene="kdtA" /locus-tag="y0086" /function="enzyme; surface polysaccharides and antigens" /note="residues 37 to 461 of 461 are 79.76 pct identical to residues 1 to 425 of 425 from E. coli K12 : B3633; residues 37 to 461 of 461 are 88.47 pct identical to residues 1 to 425 of 425 from GenPept : >gb AAC44432.1  (U52844) 3-deoxy-manno-octulosonic acid transferase [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="3-deoxy-D-manno-octuloso nic-acid transferase (KDO transferase)" /protein-id="AAM83680.1" /db-xref="GI:21956748" /translation="MNNHGSMMWCSALLAGKSLFC PDMVFLIIHINEIDRMLRLRYQV LLYLIQPLIWLRLRLSRKAPAYRKRWGERYGFC AGKVAGGIMLSVSVGETLAAIP LVRLRHRYPISLPITVTMTLPTGSERVQSAFGKD VHHVYLPYDLPGSVNRFLDQVNFK
CDS	93442..94431	
gene	94743..96128	
CDS	94743..96128	

gene	96129..96911	LVIIMETELWPNLINTLHRRKIPLVIANARLSAR SAAGYKKIGSFIRITLQIRITLIAA QNQEDGDRFIELGLKRSQTLVTGSLKFDISVTPE LAARAVTLRRQWAPHRPVWIATST HDGEETILLEAHRQLLOQFPTLLILVPRHPERF GKAVELTQKIGLSYTLRSKGEVPS SSTQVVIGDTMGELMLLYGIADLAFVGGSLVERG GHNPLEAAHAIPVLMGPHTFNFK DICAKLEQAEGELITVDTLSLVKEITVLLTDEDC RLYYGRHAVDVLHENQGAQRLLH LLEPYLPQRSH"
CDS	96129..96911	/locus-tag="y0087" /locus-tag="y0087" /function="enzyme" /note="residues 1 to 256 of 260 are 75.78 pct identical to residues 1 to 256 of 257 from GenPept : >gb AAC44433.1  (U52844) glucosyltransferase [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="lipopolysaccharide core biosynthesis glycosyl transferase" /protein-id="AAM83681.1" /db-xref="GI:21956749" /translation="MGTKRRLSVVMITKNEASLL TDCLASVAWADEIIVLDGSGSEDET RALAQQFGAKVYSNINWPGYKGQRQLAQYASGD YILMLDADERVTPELKIAIESVLL APEEGAVYSCSRRLFLGRFMRHSGWYPRDVRTL YPHHQYRYNDNLVHESLDGSAKV IPLAGDLLHLTCRDEFFAQKQLSYAEAWAIQRH QQKSCSYFAILSHTLGAFTKWL LRAGFLDGKQGLLLAVVNAQYTFNKYAALWALSH QYQKSEKS" /gene="kdtB" /locus-tag="y0088" /gene="kdtB" /locus-tag="y0088" /note="residues 1 to 159 of 159 are 73.58 pct identical to residues 1 to 159 of 159 from E. coli K12 : B3634; residues 1 to 159 of 159 are 82.38 pct identical to residues 1 to 159 of 161 from GenPept : >gb AAD28804.1  (U52844) phosphopantetheine adenyltransferase CoaD [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="putative enzyme of lipopolysaccharide synthesis" /protein-id="AAM83682.1" /db-xref="GI:21956750" /translation="MITKAIYPGTFDPITNGHLD LVTRASAMFSHVILAIADSSSKKP MFTLDERVALAKKVTAPLKNVEVLGFSELMAEFA KKHNANILVRGLSVSDFEYEWQL ANMNRHLMPKLESVFLIPSEKWSFISSSLVKEVA RHGGDITPLPKPVTKALLAKLA"
gene	96908..97387	
CDS	96908..97387	

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gene      complement(97393..98202 /gene="mutM"
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/locus-tag="y0090"
CDS       complement(97393..98202 /gene="mutM"
)
/locus-tag="y0090"
/function="enzyme; DNA -
replication, repair,
restriction/modification"
/note="residues 1 to 268 of 269
are 79.85 pct identical to
residues 1 to 268 of 269 from E.
coli K12 : B3635; residues 1 to
268 of 269 are 83.70 pct identical
to residues 1 to 270 of 271 from
GenPept : >gb|AAD28805.2| (U52844)
Fpg [Serratia marcescens]"
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/transl-table=11
/product="formamidopyrimidine DNA
glycosylase"
/protein-id="AAM83683.1"
/db-xref="GI:21956751"
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QTILYAVVRNARLRWPFVSDIILTL
SDQPVLSVQRRAKYLLLELPKGWIIHLGMSGSL
RVLSEETAEEKHDHVDLVVSNKGI
LRYTDPRRFGAWLWAKDLETSNVLAHLGPEPLSD
EFTAQYLFDKSRNKRKTIKLPWLMD
NKVVVGVGNIYASESLFAAGILPDRAAGSLTDAE
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DFLQSDGKPGYFAQELQVYGRAGEPCRQCGHPIE
IAKHGQRSTFFCRHCQH"
/locus-tag="y0089"
CDS       /locus-tag="y0089"
/note="residues 25 to 43 of 52 are
57.89 pct identical to residues
170 to 188 of 433 from GenPept :
>emb|CAB86066.1| (AL163002)
putative protein [Arabidopsis
thaliana]"
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/product="hypothetical"
/protein-id="AAM83684.1"
/db-xref="GI:21956752"
/translation="MLAVAAKERAAALPVFRYFNG
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gene      complement(98285..98452 /gene="rpmG"
)
/locus-tag="y0091"
CDS       complement(98285..98452 /gene="rpmG"
)
/locus-tag="y0091"
/function="structural component;
ribosomal proteins - synthesis,
modification"
/note="residues 1 to 55 of 55 are
96.36 pct identical to residues 1
to 55 of 55 from E. coli K12 :
B3636"
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/translation="MAKGVREKIKLVSSAGTGHF
YTTTKNKRKTPEKLELKKFDPVVR
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gene      complement(98963..99631) /gene="radC"
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CDS      complement(98963..99631) /gene="radC"
)
/locus-tag="y0092"
/function="phenotype; Not
classified"
/notes="residues 10 to 222 of 222
are 58.21 pct identical to
residues 12 to 224 of 224 from E.
coli K12 : B3638; residues 7 to
222 of 222 are 59.72 pct identical
to residues 6 to 221 of 221 from
GenPept : >gb|AAL22588.1|
(AE008873) putative DNA repair
protein, associated with
replication forks [Salmonella
typhimurium LT2]"
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/product="DNA repair protein"
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VLTDALLAIFLRTGIPGMHVMKM
AEYLIETFGSLHGLISADYQTLCAHKIGIGASKYS
QIQAI GELACRCFSSHL MRESVLL
NPGITQKFLQNILSHREREIFLVFLDNQHRVIR
HEEMFTGTISSVEVHPREIVREAL
KVNAAALILAHNHPSGKAEPSQADRLITTQVIKA
CSLLDIRVLDHLVVGRCGVSAE RGWL"
gene      99711..101042 /gene="dfp"
) /locus-tag="y0093"
CDS      99711..101042 /gene="dfp"
) /locus-tag="y0093"
/function="phenotype; DNA -
replication, repair,
restriction/modification"
/notes="residues 39 to 442 of 443
are 75.18 pct identical to
residues 23 to 429 of 430 from E.
coli K12 : B3639; residues 40 to
442 of 443 are 75.12 pct identical
to residues 1 to 406 of 407 from
GenPept : >gb|AAL22589.1|
(AE008873) flavoprotein affecting
synthesis of DNA and pantothenate
metabolism [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="flavoprotein affecting
synthesis of DNA and pantothenate

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		metabolism"
		/protein-id="AAM83687.1"
		/db-xref="GI:21956755"
		/translation="MRDVSQILRLVASESALIAN LFNGYAKISPLTAFIRTIMMTGLS GKHIVLGISGGIAAYKSPELVRRLRDKGADVRVV MTHAAKAFIAPLTLQAVSGYPVSD DLLDPAAEAAMGHIELGKWADLVIIAPATADLLA RMAAGMANDLLTTVCLATAPIAA VPAMNQOMYRAPATQENLQTLKQVLLWGPDSG SQACGDIGPGRMLDPQEIVALAYN HFSAKQDLQHLVSMITAGPTREPLDPVRFISNQS SGKMGFAIAQALAARGSNVTLIAG PVNLSTPEGVKRIDVITALEMQQAVQKIAQQQNI FISCAAVADYRAEHVSDEKIKKQG DEITLKLKPNPDIVAGVAMAKNRPFVVGFAAET QNVEYARQKLARKNLDLICANDV SLAEHGFNSDTNALHLFWSTGEKRLPLSDKYLLS QRLIDEIVSRYDEKNRH"
gene	101008..101478	/gene="dut"
		/locus-tag="y0094"
CDS	101008..101478	/gene="dut"
		/locus-tag="y0094"
		/function="enzyme; 2'-Deoxyribonucleotide metabolism" /note="residues 6 to 156 of 156 are 84.76 pct identical to residues 1 to 151 of 151 from E. coli K12 : B3640; residues 6 to 156 of 156 are 85.43 pct identical to residues 1 to 151 of 151 from GenPept : >gb AAG58784.1 AE005591-8 (AE005591) deoxyuridinetriphosphatase [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="deoxyuridinetriphosphata se" /protein-id="AAM83688.1" /db-xref="GI:21956756" /translation="MSAVMMKKIDIKILDPRVGN EFFPLPTYATEGSAGLDLRACLDHA VELQPGQTILLPTGLAIHIGDSALAAVILPRSGL GKHGIVLGNLVGLIDSDYQGQLM VSVVNRGQQPFTIEPGERIAQMVFVPVQAEFNL VEDFTDSERGTTGGFGHSGRQ"
gene	101600..102196	/gene="ttk"
		/locus-tag="y0095"
CDS	101600..102196	/gene="ttk"
		/locus-tag="y0095"
		/function="putative regulator" /note="residues 1 to 198 of 198 are 83.33 pct identical to residues 15 to 212 of 212 from E. coli K12 : B3641; residues 1 to 198 of 198 are 83.83 pct identical to residues 1 to 198 of 198 from GenPept : >gb AAL22591.1  (AE008873) putative transcriptional regulator"

```

(TetR/ArcR family) [Salmonella
typhimurium LT2]"
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QDEKETFNRLRLILLVLGFAERN
PGLTRIMTGHALMFEDQRLQGRINQLFERIEMQL
RQVLREKKLRDGGGFHDEALLAT
QLLAFCEGMLSRFVRSEFRYCPTQEFDSRWPLIV
AQLQ"
gene      complement(102331..1029 /gene="pyrE"
78)
CDS       complement(102331..1029 /locus-tag="y0096"
78)       /gene="pyrE"
          /locus-tag="y0096"
          /function="enzyme; pyrimidine
          ribonucleotide biosynthesis"
          /note="residues 1 to 213 of 215
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          residues 1 to 213 of 213 from E.
          coli K12 : B3642; residues 1 to
          213 of 215 are 85.91 pct identical
          to residues 1 to 213 of 213 from
          GenPept : >gb|AAL22592.1|
          (AE008873) orotate
          phosphoribosyltransferase
          [Salmonella typhimurium LT2]"
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          phosphoribosyltransferase"
          /protein-id="AAM83690.1"
          /db-xref="GI:21956759"
          /translation="MKAYQREFIEFALNKQVLKF
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          TTTAVALAEHHERDVPYCFNRKEA
          KTHGEGGNLVGSPLQGRVMLVDDVITAGTAIRES
          MEIINAQGATLAGVMISLDRQERG
          RGEISAIQEVERDYHCKVIAIVTLNDVIRYLEDK
          PEMAEHLVAVRQYREQYGVTL"
gene      complement(103145..1038 /gene="rph"
61)
CDS       complement(103145..1038 /locus-tag="y0097"
61)       /gene="rph"
          /locus-tag="y0097"
          /function="enzyme; degradation of
          RNA"
          /note="residues 1 to 223 of 238
          are 88.78 pct identical to
          residues 1 to 223 of 228 from E.
          coli K12 : B3643; residues 1 to
          238 of 238 are 100.00 pct
          identical to residues 1 to 238 of

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gene 103988..104851  
CDS 103988..104851

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238 from GenPept :
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/db-xref="GI:21956760"
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AKKGQGGRTLEIQRLIARSLRAAV
DLKKLGFEITITLDCDVLQADGGGTRTASISGACVA
LADALNKLVASGKLANPMKGLVA
AVSVGIVKGEALCDLEYVEDSAEETDMNVMMED
GRMIEVOGTAEGEPPFSHEELALL
DLARGGIEITIFQAQKALES"
/locus-tag="y0098"
/locus-tag="y0098"
/function="phenotype; Not
classified"
/note="residues 1 to 287 of 287
are 87.45 pct identical to
residues 1 to 287 of 287 from E.
coli K12 : B3644; residues 1 to
287 of 287 are 87.80 pct identical
to residues 1 to 287 of 287 from
GenPept : >gb|AAL22594.1|
(AE008873) putative stress-induced
protein [Salmonella typhimurium
LT2]"
/codon-start=1
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protein"
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/db-xref="GI:21956761"
/translation="MIRSMATAYARRDIKGEWGNA
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ILNEKLAKQLVEAGNWWKMQSDEG
EINPVDILRWPVGMSAEQDLDAISTELMQALDT
ALDDFIVRSRETEGAALKTLIEQRL
EGVSAEVLVVRHMPNIIQWQERLLNKLLEAAQV
QLENTREQLVLMQQRIDVAEEL
DRLEAHVKETYNILKKAEVGRRLDFMMQEFNRE
SNTLAKSINAETNSAIELKVLII
EQMREQIQNIE"
/locus-tag="y0099"
/locus-tag="y0099"
/note="residues 1 to 181 of 207
are 74.58 pct identical to
residues 19 to 199 of 223 from E.
coli K12 : B3646; residues 1 to
181 of 207 are 74.58 pct identical
to residues 19 to 199 of 223 from
GenPept :
>gb|AAG58790.1|AE005592-1
(AE005592) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1

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gene 105254..105877  
CDS 105254..105877

gene	complement (105890..107593)	/locus-tag="y0100"	/transl-table=11 /product="hypothetical protein" /protein-id="AAM83693.1" /db-xref="GI:21956762" /translation="MLLSVLYIIIGITAEAMTGA AAGRQMDMFGVIIIASATAIGGG SVRDMLLGHYPGLGWVKHPEYIVIVAIAAVITWM APLMKQLRHLFLVLDIAIGLIVFSI IGAQIALDMGHSTIIAAIAAVITGVFGVLRDML CNCIPLVFQKEIYAGISFAAAWIY IALQYTPLSHNWVIIITLITGLALDYSFYDSGLA CLYSNMSTQTIKI"
			/note="residues 6 to 564 of 567 are 43.79 pct identical to residues 3 to 561 of 562 from E. coli K12 : B3647" /codon-start=1 /transl-table=11 /product="putative enzyme" /protein-id="AAM83694.1" /db-xref="GI:21956763" /translation="MNILNKIIMFLLISNTIVV GGAWATSTCPDWPATRIAVEINAL EQQLNKWSAAYHQGGHSPVDDIYDQLQDKLRVW QSCRGLPDKTESQPIPGKGQFLHP VAHTGLKKLKDELTALTRWMAGRKNLWVQPKVDGV AVTLVYHGGKLVQLLSRGNGVKGQ NWTEKAPFISAIPQYIANAPALLTQGEFLFLMD GHQQAQSGGVNARSTVAGALMRKS PSPLLAQGVVF INAWPDGPTTMEKVALLVQMGF PFTAKYSEPVMSHLDVVQWRQFWF QAPLPFVITDGVVVRQEEEPAGRYWQATPGQWSMA WKYPLPQHIAEVKDIHFTLGRGTGK GTVVLEVLPKIDDKWIRRVNIGSVTRWKQWDIA PGDHITLALAGHGIPRLDNVVRV HORNTITAPNWDFHQLSCFQRLPHGCEPQFLSR LIWLSGPGGLDIGGIGGGFWQELI HHLEINDLVGWLTLTPEQIASIPGIGNARAEKIY QQFQRAKQPPFSRWLLALGPPQV SVDAQVQVVLRRRLSEWATMAGIGQMRKQIKHF LDHPDVQALADFLSTQKVVGFEIT E"
gene	107994..108617	/locus-tag="y0101"	/gene="gmk" /locus-tag="y0101" /function="enzyme; purine ribonucleotide biosynthesis" /note="residues 1 to 207 of 207 are 87.92 pct identical to residues 1 to 207 of 207 from E. coli K12 : B3648" /codon-start=1 /transl-table=11 /product="guanylate kinase" /protein-id="AAM83695.1" /db-xref="GI:21956764" /translation="MVQGTLYIVSPAGSAGKSSL IOALLKTOPLYDPTOVSIHTTRAK

gene 108672..108947

CDS 108672..108947

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ENYGTGSRLAIEQVLATGVDVFLD
IDWQGAQQIRAKMPTARSIFILPPSKTELDRLRL
GRGQDSEEVIAKRMEQAVAEAMAHY
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QRHDALISKLLAD"
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/locus-tag="y0102"
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/locus-tag="y0102"
/function="enzyme; RNA synthesis,
modification, DNA transcription"
/note="residues 1 to 91 of 91 are
92.30 pct identical to residues 1
to 91 of 91 from E. coli K12 :
B3649"
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/transl-table=11
/product="RNA polymerase, omega
subunit"
/protein-id="AAM83696.1"
/db-xref="GI:21956765"
/translation="MARVTVDQAVEKIGNRFDLV
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gene 108967..111075
CDS 108967..111075
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/locus-tag="y0103"
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/locus-tag="y0103"
/function="enzyme; global
regulatory functions"
/note="residues 1 to 702 of 702
are 91.45 pct identical to
residues 1 to 702 of 702 from E.
coli K12 : B3650; residues 1 to
702 of 702 are 91.89 pct identical
to residues 1 to 703 of 703 from
GenPept : >gb|AAL22601.1|
(AE008874) bifunctional : (p)ppGpp
synthetase II; also
guanosine-3',5'-bis pyrophosphate
3'-pyrophosphohydrolase
[Salmonella typhimurium LT2];
guanosine-3',5'-bis pyrophosphate
3'-pyrophosphohydrolase"
/codon-start=1
/transl-table=11
/product="(p)ppGpp synthetase II"
/protein-id="AAM83697.1"
/db-xref="GI:21956766"
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LDKLNFRDKKEAQAEFRKMIMAMVQDIRVILIK
LADRTHNMRTLGLSLRPDKRRRIAR
ETLEIYSPLAHLRGLIHHLKTEELGFEALYPNR
YRVIKEVVKAARGNRKEMIQKILA
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LGQAHS�YKPRGRVKDYIAIPKANGYQSLHTSL
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gene	111081..111773	/gene="spoU"
		/locus-tag="y0104"
CDS	111081..111773	/gene="spoU"
		/locus-tag="y0104"
		/note="residues 1 to 227 of 230 are 82.81 pct identical to residues 1 to 227 of 229 from E. coli K12 : B3651"
		/codon-start=1
		/transl-table=11
		/product="putative RNA methylase"
		/protein-id="AAM83698.1"
		/db-xref="GI:21956767"
		/translation="MNPQRYARICDMLATRQPD LTVCLQVHKPHNVSAIIRTADAVG IHQVHAIWPTTQMYTRLSSAAGSNWVQVKTHP IADAIAIYLSQDMQILATHLSDKA VDFREIDYTRPTCILMGOEKTGISPEALALADQD IIIPMIGMVQSLNVSVASALILYE AQRORQNAAGMYKRTHSVLAESEQRLLFEGGYPV LAHVAKRKGLPQPHIDEQQGQIIAD AQWWSAMQATES"
gene	111774..113855	/gene="recG"
		/locus-tag="y0105"
CDS	111774..113855	/gene="recG"
		/locus-tag="y0105"
		/function="enzyme; DNA - replication, repair, restriction/modification"
		/note="resolution of Holliday junctions, branch migration; residues 1 to 693 of 693 are 81.52 pct identical to residues 1 to 693 of 693 from E. coli K12 : B3652; residues 1 to 693 of 693 are 81.24 pct identical to residues 1 to 693 of 693 from GenPept : >gb AAL22603.1  (AE008874) DNA helicase, resolution of Holliday junctions, branch migration [Salmonella typhimurium LT2]"
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		/transl-table=11
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		/protein-id="AAM83699.1"
		/db-xref="GI:21956768"
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 AEEQLKQRFALALPPTPTQAQQRV  
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 TATPIRPTLAMTAYADLDTSVIDE  
 LPPGRTPVTTVAIPDTRRSVDIQRVKNACLEEGR  
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 EELKIALPEIKVGLVHGRMKGPEKQAIMLAFKQG  
 ELQLLVATTVIEVGVDPVFNASLMI  
 IDNPERLGLAQLHLQLRGRVGRGAVASHCVLLYKT  
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gene complement(114221..1154  
 35)

CDS complement(114221..1154  
 35)

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 /function="transport; transport of  
 small molecules; amino acids,  
 amines"  
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 are 82.45 pct identical to  
 residues 1 to 399 of 401 from E.  
 coli K12 : B3653; residues 1 to  
 399 of 404 are 82.45 pct identical  
 to residues 1 to 399 of 401 from  
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 (AJ005339) glutamate permease  
 [synthetic construct]"  
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 AGSITLSG GHGTGAWSKLPSEYGFENATE  
 VAMACATFGLVLGGLIGGPVARYLVKHS  
 STPEGTP DDSAVPSAFEKPSAGRMITSL  
 VLIETIAMISICLMAGNLIAAGLQGTMF  
 FELPIFVCVLFVGVIISNTLSASGFYR  
 VFDRAVSVLGNVLSLSFLAMALMSLKL  
 WELASLALPMLVILSVQALAMALYAI  
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CDS	115622..117058	/locus-tag="y0107"
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		/note="residues 18 to 478 of 478 are 83.98 pct identical to residues 1 to 462 of 463 from E. coli K12 : B3654; residues 18 to 478 of 478 are 83.76 pct identical to residues 1 to 462 of 463 from GenPept : >gb AAL22606.1  (AE008874) putative NCS2 family, purine/xanthine transport protein [Salmonella typhimurium LT2]"
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		/transl-table=11
		/product="putative transport protein, symporter"
		/protein-id="AAM83701.1"
		/db-xref="GI:21956771"
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gene	117206..118915	/locus-tag="y0108"
CDS	117206..118915	/locus-tag="y0108"
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		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83702.1"
		/db-xref="GI:21956772"
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HQWGVWSGSLVLNAGNATFNKNDI  
 RRPSSLALNANEQQITFSDLSAPTKEGLLEATASI  
 DQTPDRALSLALTGRSDVLNLFHN  
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gene complement(119050..11973) /locus-tag="y0109"  
 CDS complement(119050..11973) /locus-tag="y0109"  
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 RHFLMIKPVATMDDILHRPWCQO  
 LQQAWYDHIPLSEKMGVRISQYTGQRFVITMPEA  
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 gene 120608..121261 /locus-tag="y0110"  
 CDS 120608..121261 /locus-tag="y0110"  
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 putative transposase [Yersinia pestis]"  
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 DVETANRHGLRWLHDVANQRKHET  
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 CDS 121258..122040 /locus-tag="y0111"  
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 /note="IS100; orfB; residues 1 to 260 of 260 are 100.00 pct

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identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
[Yersinia pestis]"
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DFTFATGAPQKQLQSLRSLSFIER
NENIVLLGPGSGVGKTHLAIAMGYEAVRAGIKVRF
TTAADLLQLSTAQRGRYKTTLQ
RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAGR
YEKSAMILISNLPFGQWDQTFAGD
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VIAEANPE"
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/note="residues 18 to 310 of 311
are 77.81 pct identical to
residues 35 to 327 of 328 from E.
coli K12 : B3102"
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YLRAAPDYSGRVTVPVLWDKQQQTVVSNESADII
RMFNNAFDDVGAKAGDYPTALRN
DIDDINGVYDQVNNGVYKAGFATTQEAYDEAVG
TLFSALDRLEQLGQHRYLTGNQL
TEADRLRLWTTLVRFDPVYVTHFKCDKRRISDYPN
LYGFLRDIYQMPGIAETVDFAHIR
THYYSRSHGTINPYGIISIGPQQLLEPHDRANRF
V"
gene      complement(123122..1240 /locus-tag="y0113"
15)
CDS       complement(123122..1240 /locus-tag="y0113"
15)

/function="putative regulator"
/note="residues 1 to 294 of 297
are 89.45 pct identical to
residues 1 to 294 of 298 from E.
coli K12 : B3105"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator LYSR-type"
/protein-id="AAM83707.1"
/db-xref="GI:21956777"
/translation="MARDRALTEALRVMDAIDR
RGSFAAADELGRVPSALSYSYTMQK
LEELDVVLFDRSGHRTKFTNVGRMLLERGRVLL
EAADKLTTDAEALARGWETHITIV
SEALSPAWKFLPLIDKLANKANTQVSILTEVLG

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AWERLEQGRADIVIAPDMHFRASS
EINSRKLYKVTSVYVASPDHPHIOHEPEPLSELTR
VKYRGIAVADTARERPVITVQLLD
KQQRLLTVSTIEDKRRALLAGLG VATMPYEMVEKD
IAAGRLRVIGPEYSREADIIMAWR
RDSMGEAKSWCLREIPKLLGK"
gene      complement(124135..1242 /locus-tag="y0114"
84)
CDS       complement(124135..1242 /locus-tag="y0114"
84)
/locus-tag="y0114"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83708.1"
/db-xref="GI:21956779"
/translation="MIMTMITSYTGHLSHRKES
VGLSIGSPLODCGNRFSTRLSFVG RFPES"
gene      124277..124981 /locus-tag="y0115"
CDS       124277..124981 /locus-tag="y0115"
/locus-tag="y0115"
/note="residues 1 to 234 of 234
are 68.80 pct identical to
residues 1 to 233 of 233 from E.
coli K12 : B3106; residues 1 to
234 of 234 are 71.79 pct identical
to residues 1 to 233 of 233 from
GenPept : >emb|CAD07760.1|
(AL627278) conserved hypothetical
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83709.1"
/db-xref="GI:21956780"
/translation="MITCRTAEQCGQADFGWLQA
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QEVLPAGAAFPQRTYPQVDILNLILQGEAEYRDS
LGNHVHAKTGDALLFSPOQGVSY
EHNLSANKSLTRIQLWLNACPERESAPTQHQRLS
TRPVQLLASPAGEQGSLLRLRQQM
IHHLAALAGEQKQKMLHGHRAYLQSIHGTVDATG
PQTGTSQRLTCGDGAFVEEQHLV
IKAITPLRALLIDLVP"
gene      complement(125522..1258 /locus-tag="ys001"
98)
misc-RNA  complement(125522..1258 /locus-tag="ys001"
98)
/locus-tag="ys001"
/product="RNase P, RNA component"
/note="M1 RNA; processes tRNA"
/function="RNA; Macromolecule
degradation: Degradation of RNA"
/locus-tag="y0116"
gene      125522..125890 /locus-tag="y0116"
CDS       125522..125890 /locus-tag="y0116"
/locus-tag="y0116"
/note="residues 82 to 114 of 122
are 48.48 pct identical to
residues 47 to 79 of 271 from
GenPept : >dbj|BAB31852.1|
(AK019785) data source:SPTR,
source key:Q9NQV8, evidence:ISS
homolog to PR-domain containing
protein 8 putative [Mus musculus]"
/codon-start=1

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/transl-table=11
/product="hypothetical"
/protein-id="AAM83710.1"
/db-xref="GI:21956781"
/translation="MELTGKPGSVVDSDSHSRPAI
AHLWKQPTRVQYGPYHANPYLALL
RVFETMPRTVASRAVRSYRTLSPLEDPCTCVGHRH
FALCCTCRRLLAPRRRYLAPCPMEP
GLSSPPFPVSPERDGEAAATV"
/locus-tag="y0117"

gene      complement(125918..1268
17)
CDS       complement(125918..1268
17)

/note="residues 1 to 286 of 299
are 85.31 pct identical to
residues 1 to 285 of 286 from E.
coli K12 : B3146"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83711.1"
/db-xref="GI:21956782"
/translation="MNQHDRAVISASTLYVVPFP
IGNLGDITRALEVLKGVDLIAAE
DTRHTGLLQLQHFAINARLFAHLDHNEQQKADQLL
AKLQEGQSIALVSDAGTFLINDPG
YHLVRRRCREAGIRVVPLPGACAAITALSAGLAS
DRFCYEGFLPAKTKGRKDTLQALI
EEPTLILFYESTHRLLESLDQMTVLGPPQRYVVL
ARELTKTWESIHGAPVGELLAWVK
EEETRRRGEMVLIVEGHKVQSDDALPADALRTLIA
LLQKELPLKKAALAAEIHGVKKN
ALYKYALEQQQGDVETEEDDIQQ"
/locus-tag="y0118"
/locus-tag="y0118"
/note="residues 33 to 689 of 689
are 53.00 pct identical to
residues 1 to 678 of 678 from E.
coli K12 : B3147; residues 33 to
687 of 689 are 55.99 pct identical
to residues 1 to 678 of 680 from
GenPept : >gb|AAL22136.1|
(AE008850) paral putative
transglycosylase [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="putative glycosylase"
/protein-id="AAM83712.1"
/db-xref="GI:21956783"
/translation="MQKLLLDREVDSLPHNYRFN
IEHLEKNI TGYSMLSTFVRSKAG
LVPVILAAALILAACTGDAPQTPTPPVNIQDEASAN
SDYYLQQLQSSSDNKADWQLLAI
RALLREAKVPQAAEQSLTLPANLSDTQRQEQLL
AAELLLIAQKNTPTAAADILAKLEAT
QLSANQKVRYYQAQIAANQDKATLPLIRAFIAQE
PLLTDKAHQDNI DGTWQSLTLP
QELNTMVINADENVLQGWLLDLRLVYQDNKQDPEL
LKAGIKDWQTRYRPNPAAKNLPPTA
LTQISNFSQASTAKIALLLPLSPGAQVFADAIQQ
GFTAAONGSAVTASVPVTPNVTES

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SPTDTAAVSDDTPATLPAPVPPVVTNAQVKIY  
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 CYFALSPEDEARDAHHLWEQQKR  
 MPLLLVPRGALGERIAKAFADQWQKGGQTVLQQ  
 NFGSTTELKQSSINGAGIRLTGTPT  
 VSVSNVAAAPASVTIAGLTIPAPPIDAPVVSTSS  
 SGNIDAVYIIATPSELTLIKPMID  
 MATSSRSKPALFASSRSYQAGAGPDYRLEMEGIQ  
 FSDIPLMAGSNPALLQQASAKYAN  
 DYSLVRLYAMGIDAWALANHFSEMRQIPGFQVKG  
 VTGDLTASSDCVITRKLPLWLYRQ GMVPLA"  
 /locus-tag="y0119"  
 /locus-tag="y0119"  
 /note="residues 1 to 115 of 117  
 are 57.39 pct identical to  
 residues 14 to 128 of 131 from E.  
 coli K12 : B3148; residues 1 to  
 115 of 117 are 57.39 pct identical  
 to residues 14 to 128 of 131 from  
 GenPept : >gb|AAL22137.1|  
 (AE008850) putative endonuclease  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
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 /db-xref="GI:21956784"  
 /translation="MSQRDTGAHYENLARRHLER  
 AGLVFQAANVAFRGGEIDLIMRDG  
 DAWVFVEVFRFRNDLFGGAASITPRKQQRHLHLA  
 AAVWLAQRGASFATTSCRFDVVAI  
 TGNQLEWLPNAFNND"  
 /locus-tag="y0120"  
 /note="residues 3 to 49 of 126 are  
 37.99 pct identical to residues  
 674 to 722 of 1684 from GenPept :  
 >gb|AAC27151.1|AAC27151 (AC004512)  
 Similar to gb|U46691 putative  
 chromatin structure regulator  
 (SUPT6H) from Homo sapiens. ESTs  
 gb|T42908, gb|AA586170 and  
 gb|AA395125 come from this gene.  
 [Arabidopsis thaliana]"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical"  
 /protein-id="AAM83714.1"  
 /db-xref="GI:21956785"  
 /translation="MLFKLVDPQFFSRLPSACNS  
 NYLGIARYQLENKHQSVLKALGSH  
 SNWLPIVATTSKRQDVVAKLAPRCASQTAAARCS  
 RCCLRGVILAAAPPNRSRLRRKRTS  
 TNTHASPSRIIRSISPPRKATLAA"  
 /locus-tag="y0121"  
 /note="residues 2 to 25 of 28 are

gene	128937..129290	
CDS	128937..129290	
gene	complement(129011..129391)	
CDS	complement(129011..129391)	
gene	complement(129415..129501)	
CDS	complement(129415..129501)	

gene	129561..130151	50.00 pct identical to residues 839 to 862 of 1165 from GenPept : >gb AAD10500.2  (U53471) receptor tyrosine kinase proto-oncogene [Xiphophorus xiphidium]"
CDS	129561..130151	/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83715.1" /db-xref="GI:21956786" /translation="MVTLLNNPNHLLVVDFKVS KSLIGINEPYP" /locus-tag="y0122" /locus-tag="y0122" /note="residues 1 to 196 of 196 are 93.36 pct identical to residues 1 to 196 of 196 from E. coli K12 : B3149" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83716.1" /db-xref="GI:21956787" /translation="MLERIKGCFTESIQTI AAAEALPDATSCAAMALVQSLNNGKI LCCNGTISAANAQHFASMINRFETERP SLPAIALNADNVVLTAITNDRLHDEVYAKQ VRALGQAGDVLIAISTRGNSRDIVKAVEA AVTRDMTIVALTGVDGGELAGLLGQLDVE IRIPSHRGARVQELHMLTVNCLDLIDNT LFPHQND" /locus-tag="y0123" /locus-tag="y0123" /function="putative transport" /note="residues 16 to 206 of 206 are 73.29 pct identical to residues 1 to 191 of 191 from E. coli K12 : B3150; residues 16 to 206 of 206 are 73.82 pct identical to residues 1 to 191 of 191 from GenPept : >gb AAL22139.1  (AE008850) paral putative periplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="conserved putative exported protein" /protein-id="AAM83717.1" /db-xref="GI:21956788" /translation="MTTLYFLIRTIKGAP MKVGYIFAMLFSTLLQGCGVAVVVGSA AVATKTAIDPTRTIGTQVDDGILEARV VNALSKDKEIKSQTRFVVTA YQGVLLTGQTPSAELSNRAKQIASG VDGVTEVYNEMRLGKPVDLST ASMDTWITTKVRSQLLTSDSVKSS NVKVTTENGEVFLGLVTQGEAQSA AQIASKVSGVKHVTTAFTIVK"
gene	130117..130737	
CDS	130117..130737	
gene	complement(130944..131669)	/gene="mtgA"
CDS	complement(130944..131669)	/locus-tag="y0124" /gene="mtgA"

69)

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/locus-tag="y0124"
/note="residues 17 to 241 of 241
are 72.44 pct identical to
residues 18 to 242 of 242 from E.
coli K12 : B3208"
/codon-start=1
/transl-table=11
/product="putative peptidoglycan
enzyme"
/protein-id="AAM83718.1"
/db-xref="GI:21956789"
/translation="MISVRRGFSQLWYWGKRGVI
GIIALWMAGILIFAFLPVPFSMVM
IERQLGAWLTGDFAYVAHSDWVPMDEISPYMALA
VMAAEDQKFFPDHWGFDVGAIESAL
SHNQRNQKRIGASTLSQQTAKNVFLWDGRSWSVR
KGLEVGLTAGIELIWKRRILTVY
LNIAEFGNGIFGVAAAARHFFNKPASKLSASEAA
LLAAVLPNPLRFKVNAPSGYVISR
QQWILRQMHQLGGKTFLLQENTLD"
/locus-tag="y0125"
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gene complement(131666..1323  
19)

CDS complement(131666..1323  
19)

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/function="putative factor"
/note="residues 1 to 217 of 217
are 63.59 pct identical to
residues 4 to 220 of 220 from E.
coli K12 : B3209; residues 1 to
217 of 217 are 65.89 pct identical
to residues 1 to 217 of 217 from
GenPept : >emb|CAD07844.1|
(AL627278) conserved hypothetical
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="sigma cross-reacting
protein 27A (SCRP-27A)"
/protein-id="AAM83719.1"
/db-xref="GI:21956790"
/translation="MKTVGVVLSGCGVLDGAEIH
ESVLTMLALDRAGAELVFFAPDKP
QLHVINHITGEIVAEERNVLVESARIARGLITPL
SAADPEVLDALIVPGGFGAAKNLC
DFAIKGGECSEVPDLYKLIQLMHKSGKPIGLMCI
SPVMLPKLLGKPIRLTIGNDPDTI
DAIEIMGGEHVICPADDVVIDLENKVVTTPAYML
AGSISEAAKGIDKLVTKVLDLTE"
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gene complement(132561..1348  
97)

CDS complement(132561..1348  
97)

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/locus-tag="y0126"
/genes="arcB"
/locus-tag="y0126"
/function="enzyme; global
regulatory functions"
/note="sensor for arcA; residues 1
to 778 of 778 are 75.92 pct
identical to residues 1 to 776 of
776 from E. coli K12 : B3210;
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residues 1 to 778 of 778 are 77.33  
 pct identical to residues 1 to 778  
 of 778 from GenPept :  
 >gb|AAL22197.1| (AE008853) sensory  
 histidine kinase in two-component  
 regulatory system with Arca,  
 senses redox conditions  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="aerobic respiration  
 sensor-response protein; histidine  
 protein kinase/phosphatase"  
 /protein-id="AAM83720.1"  
 /db-xref="GI:21956791"  
 /translation="MKQIRVLAQYYVDLMVKLGL  
 VRFSLLLASALVLLAMVVQMAVTF  
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 QLEESRQRLSRLVDKLEVMRHRDL  
 ELNKQLTENITQLNQIEVEREKAHAHLQVVDKL  
 KEEMGHREQAQIELGQQSALLRSF  
 LDASPDLVYYRNEDNEFSGCNRAMELLTGKSEKQ  
 LVGLTPKDVYAPDIAEKVMTDEK  
 VFRHNVSITYEQWLVIYDPGRKACFELRKVPFYDR  
 VGRHGLMGFGRDITERKRYQDAL  
 ENASRDKTTFISTISHELRIPLNGIVGLSRILLD  
 TELDAEQKLYLKTIVHSAITLGNL  
 FNDIEMDKLERRKVQLDNQVPDFTGFMADLENL  
 SGLLVQPKGLKFIMEPQLPLPEKV  
 IADGTRLRQILWNLIGNAVKFTQQGKIVVRVRE  
 GNDRLIFEVEDSGMGIPEDQDKI  
 FAMYYQVKDRNGGRPATGTGIGLAVSKRLAQSMG  
 GDITVKSTQGVGSCFTLTIKAPAV  
 QEASNAFSGDDMPLPALHVLVVEDIELNVIVARS  
 VLEKLGNSVDVAMNGHDALAMFNP  
 EDFDLVLLDIQLPDMSGLDIARQIRAEYGKQSLP  
 PLVALTANVLKDKKEYLDAGMDVV  
 LSKPLSVPALTAMIKQFWDSPSSAVQKQEHKVM  
 QTHESLLDTTMLEQYIDLVGQPLI  
 HQSLEMFEQMMPGYLAVLDSNMTARDQKGITEEA  
 HKIKGAAGSVGLRHHIQQLAQOIQT  
 PTLPAWWDNVQDWDVDELKLEWRNDVQVLEWAAE  
 VEKK"

gene complement(135161..1361 /locus-tag="y0127"  
 50)

CDS complement(135161..1361 /locus-tag="y0127"  
 50)

/note="residues 23 to 323 of 329  
 are 78.73 pct identical to  
 residues 1 to 301 of 309 from E.  
 coli K12 : B3211"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical protein"  
 /protein-id="AAM83721.1"  
 /db-xref="GI:21956793"  
 /translation="MLLGRNANGFGYGLFLTGSA  
 KIMQLQQLVNMFGADLQRRYGEKI  
 HKLTLHGGFSCPNRDGLGRGGCTFCQVASFADE  
 QMQQQSITQQLAIQAKKANRANRY  
 LAYFQAYTSTYAEVNALAMYQQALCEADIVGLC  
 VGRTPDCVPAVDLLSSYQQQY"

gene 136757..141364

CDS 136757..141364

EVWLELGLQTANDKTLKRINRGHDFACYQQTARR  
ARARGLKVCCHLIVGLPGEDRAQG  
RETLEKVVTTGVDGIKLHPLHIVEGSTMAKAWRA  
GRLTALALEDYVLTAGEMIRHTPA  
EVVYHRISASARRPTLLAPLWCENRWTGMNELNN  
YLLQHGVQGTAGDAYCYR"  
/gene="gltB"  
/locus-tag="y0128"  
/gene="gltB"  
/locus-tag="y0128"  
/function="enzyme; central  
intermediary metabolism: Pool,  
multipurpose conversions"  
/note="residues 43 to 1535 of 1535  
are 87.55 pct identical to  
residues 24 to 1517 of 1517 from  
E. coli K12 : B3212; residues 51  
to 1535 of 1535 are 89.23 pct  
identical to residues 1 to 1486 of  
1486 from GenPept :  
>gb|AAK94787.1| (AY035435)  
glutamate synthase large subunit  
[Klebsiella aerogenes]"  
/codon-start=1  
/transl-table=11  
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large subunit"  
/protein-id="AAM83722.1"  
/db-xref="GI:21956794"  
/translation="MRTITRGHWRRAEKQICRKA  
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DGCGLLLQKPDHFFRMVAERGWRLAKNYAVGMM  
FLSQDEELAKASRRIVEEELQNET  
LSIVGWREVPTNPDLVGEIALSSLPRIEQIFVNA  
PAGWRSRDMERRLFVARRRIEKRI  
SDKDFYACSFNSLVTIYKGLCMPADLPRFYLDLA  
DLRLESAICLFHQRFSTINTVPRWP  
LAQPFRYLAHNGEINTIAGNRQWAKARAYKFKTP  
LIPDLQDAAPFVNETGSDSSSLDN  
MLELFLSGGMDLIRAMRLLVPPAQQNNPMDMDTL  
RAFFDFNSMHMEFPWDGPAGIVMSD  
GRYAACNLDRNGLRPARYVITKDKLITCASEVGI  
WDYQPEDEVVEKGRVGPGLMVIDT  
RSGKILHSAETDNDLKSRRHPYKEWMEKNVKRLVP  
FEDLPPEEQVGSRLQDDSOLETYQK  
QFGYSNEELDQIIRVLGENGQEATGSMGDDTPFA  
VLSSGPRIIYDYFRQQFAQVNTNP  
IDPLREAHVMSLATSIGREMNVFCEAEGQAHRLS  
FKSPILLYSDFQQLTTLLEGHYRA  
DRDLTFNPAENDLEQAVLSLCEAERKVRDGAV  
MLVLSDRAIAPNRLPVPAPMAVGA  
IQTRLVDKSLRCDANIIVETASARDPHHFAVLG  
FGATAIYPYLAYESLAKLVDSQAI  
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YRCACLFEAVGLHRDLSLDCFGQGV  
SRIGGASFSDFQODLQNLKRAWLKRKPLDQGG  
LKFVHNGEYHAYNPVVSTLQKAV  
HSGEYSDYQAYAKLVNERPIATLRDLIAIKPQGT  
PIPVQVPEAESLFKRFDTAAMS  
I  
GALSPEAHESLAIAMNSLGGSNSGEGGEDPARY

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GTNKVSRIKQVASGRFGVTPAYLV
NADVIQIKVAQGAKEGGGQPGDKVTPYIAKLR
YSVPGVTILISPPPHDDIYSIEDLA
QLIFDLKQVNPKAMISVKLVSEFGVGTIATGVAK
AYADLITIAGYDGGTGASPLSSVK
YAGCPWELGLVETQQAALVANGLRHKIRLQVDGGL
KTGVDIVKAAAILGAESFGFGTGPM
VALGCKYLRIHLNNCATGVATQDEKLRRDHYHG
LPERVVNYFHFIAETREIMAELE
VSQVLDLIGRTDMLLELDGISAKQNKLDLSPMLK
TATPHPGKALYCTESNPPFDKGLL
NKELLSQLAEPYIEAKQSKTFYFDIRNTDRSVGAA
LSGAIATKHGDQGLATDPIKAYFS
GTAGQSGFVWNAGGVLEMLTGDANDYVKGGMAGG
RIAVRPPVGSNFRSHEASIIIGNTC
LYGATGGKLFAGRAGERFAVRNSGAIIVVEGIG
DNGCEYMTGGIIVCVLGRGTINFGA
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ELRVQAQ"
gene      141374..142792 /gene="gltD"
CDS       141374..142792 /locus-tag="y0129"
                               /gene="gltD"
                               /locus-tag="y0129"
                               /function="enzyme; central
                               intermediary metabolism: Pool,
                               multipurpose conversions"
                               /note="residues 1 to 472 of 472
                               are 84.32 pct identical to
                               residues 1 to 472 of 472 from E.
                               coli K12 : B3213; residues 1 to
                               472 of 472 are 84.74 pct identical
                               to residues 1 to 472 of 472 from
                               GenPept : >gb|AAK94788.1|
                               (AY035435) glutamate synthase
                               small subunit [Klebsiella
                               aerogenes]"
                               /codon-start=1
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                               small subunit"
                               /protein-id="AAM83723.1"
                               /db-xref="GI:21956795"
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                               LCEGSCITLNDIEFGAVTIGNIERYISDKAIAMGWK
                               PDMSHVHPTGKRVAIVIGAGPAGLA
                               CADVLARNGVQAVVDRHPEIGGLLTFGIPAFKL
                               EKEVMIKRRKIFSEMGIEFOLNTE
                               VGKDITMEALLKDYDPVFLGVGTYQSMRGGLENE
                               EANGVYDALPFLIANTRQLMGYEA
                               TAHEPYINMQGKRVVVLGGGDAMDCVRSSIRQG
                               ATDVVCAYYRRDEVNMPGSKREVKN
                               AREEGVEFFKFNLPQLSIEVNSNGKVCGRVMVRTQ
                               LGAPDAQGRRMAEQIPGSEHVLPA
                               DAVVMAFGFRPHSMEWLAADHKLDKQGRVIAPE
                               STDNAFQTSNPKIFAGGDIVRGSD
                               LVVTAIAEGRKAADGIMNYLEV"
gene      143233..143718 /locus-tag="y0130"

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CDS	143233..143718	/locus-tag="y0130" /note="residues 22 to 72 of 161 are 33.33 pct identical to residues 2690 to 2740 of 3744 from GenPept : >gb AAB68923.1  (U00060) TraIp [Saccharomyces cerevisiae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83724.1" /db-xref="GI:21956796" /translation="MKFHLFFIVGGLLAMSSSAF AMSLNYQEVGVNIEARGARAVVAE LEKSGQLPAVENNIKLGDDNWIAMAPKLASAGNP KFTGVKSALESSALIYNPAAVLKA VSGSKILTLSDVCTAPIDVKDSEAKANFQQRASR TLLTIKNSDMAGPRDSCLAELKKL S" /gene="sspB"
gene	complement(143871..144386)	
CDS	complement(143871..144386)	/locus-tag="y0131" /gene="sspB"  /locus-tag="y0131" /function="regulator; global regulatory functions" /note="residues 1 to 171 of 171 are 72.51 pct identical to residues 1 to 165 of 165 from E. coli K12 : B3228" /codon-start=1 /transl-table=11 /product="stringent starvation protein B" /protein-id="AAM83725.1" /db-xref="GI:21956797" /translation="MEMSDMSPRRPYLLRAFYEY LIDNQLTPHLVVDVTRPGVSVPM FARDDGQIVLNVAAPRAVGNLELSDDDVRFNARFGG VPRQVTVPIAAVMAIYARENGSGT MFEPEAAAYDADADGNFEGIEGKETAPTIESML VTDDTRVEQDDDNSPDDKPPQPPR SGGRPALRVVK" /gene="sspA"
gene	complement(144392..145033)	
CDS	complement(144392..145033)	/locus-tag="y0132" /gene="sspA"  /locus-tag="y0132" /function="regulator; global regulatory functions" /note="residues 1 to 209 of 213 are 83.73 pct identical to residues 1 to 209 of 212 from E. coli K12 : B3229; residues 1 to 213 of 213 are 100.00 pct identical to residues 1 to 213 of 213 from GenPept : >emb CAC92790.1  (AJ414157) putative stringent starvation protein A [Yersinia pestis]" /codon-start=1 /transl-table=11

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        /product="regulator of
        transcription; stringent
        starvation protein A"
        /protein-id="AAM83726.1"
        /db-xref="GI:21956798"
        /translation="MAVAANKRSVMTLFSGPTDI
        FSHQVRIVLAEKGSVEIEQVEAD
        NLPQDLIDLNPYRTVPTLVDRELTLYESRIIMEY
        LDERFFPHPLMPVYPVARGSSRLM
        MHRIEHDWYSLLYKIEQGNQAEAEARKQLREEL
        LSIAPVFNETPFFMSEEFSLVDCY
        LAPLLWRLPVLGIEFTGAGSKELKGYMTRVFERD
        AFLASLTEAEREMHLKTRS"
gene      complement(145407..1458 /gene="rpsI"
05)
CDS       complement(145407..1458 /locus-tag="y0133"
05)       /gene="rpsI"
        /locus-tag="y0133"
        /function="structural component;
        ribosomal proteins - synthesis,
        modification"
        /note="residues 3 to 132 of 132
        are 92.30 pct identical to
        residues 1 to 130 of 130 from E.
        coli K12 : B3230; residues 3 to
        132 of 132 are 93.07 pct identical
        to residues 1 to 130 of 130 from
        GenPept : >gb|AAL22213.1|
        (AE008854) 30S ribosomal subunit
        protein S9 [Salmonella typhimurium
        LT2]"
        /codon-start=1
        /transl-table=11
        /product="30S ribosomal subunit
        protein S9"
        /protein-id="AAM83727.1"
        /db-xref="GI:21956800"
        /translation="MAMAENQYYGTRRKSSSAR
        VFLKPGSGKIVINQRSLEVYFGRE
        TARMVVNQPLELVDVMVKFDMYITVKGGGISGQA
        GAIIRHGITRALMEYDESLRGLRK
        AGFVTRDAREVERKKVGLRKARRRPQFSKR"
gene      complement(145814..1462 /gene="rplM"
57)
CDS       complement(145814..1462 /locus-tag="y0134"
57)       /gene="rplM"
        /locus-tag="y0134"
        /function="structural component;
        ribosomal proteins - synthesis,
        modification"
        /note="residues 6 to 147 of 147
        are 95.07 pct identical to
        residues 1 to 142 of 142 from E.
        coli K12 : B3231"
        /codon-start=1
        /transl-table=11
        /product="50S ribosomal subunit
        protein L13"
        /protein-id="AAM83728.1"
        /db-xref="GI:21956801"

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/translation="MGKLLMKTFTAKPETVKRDW
YVVDASGKTLGRLATELARRLRGK
HKAETYTPHVDTDGYIIIVLNAEKVAVTGNKRTDKI
YYHHTGFVGGIKQATFEEMIARRP
ERVIEIAVKGMLPKGPLGRAMYRKLVYAGTEHN
HAAQQPOVLDI"
gene      complement(146556..1476 /locus-tag="y0135"
95)
CDS       complement(146556..1476 /locus-tag="y0135"
95)

/note="residues 5 to 378 of 379
are 64.97 pct identical to
residues 1 to 373 of 375 from E.
coli K12 : B3232; residues 5 to
379 of 379 are 66.66 pct identical
to residues 1 to 374 of 374 from
GenPept : >gb|AAL22215.1|
(AE008854) putative ATPase
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83729.1"
/db-xref="GI:21956802"
/translation="MRINMQSSPITLYQQALDA
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QYQNVPAASASLRNLRGLFGKPARPPVSPVQG
LYMGGVGRGKTWMLDFFHSLPG
ERKLRLHFRHFRMLRVHQELTELQGHENPLEIVAD
GFKAQTDVLCFDEFFVSDITDAML
LATLLEALFARGITLVATSNIPFDNLYHNLQRG
RFLPAIALIKQHCEVMNVNVDAGIDY
RLRTLQANLYLTPINSQTEQAAIAIFVKLAGKE
GKGATVLEVNHRPLPAICVAEGLV
AVDPHTLCBEARSQLDYIALSKRYHTVLLHNVR
MAARDENTARRFLALVDEFYERRV
KLIIAAEASMFETIYSGERLKFYQRCLSRLEQEMQ
SEELYLSLPHLP"
/locus-tag="y0136"
/locus-tag="y0136"
/note="residues 1 to 127 of 134
are 80.31 pct identical to
residues 3 to 128 of 134 from E.
coli K12 : B3233; residues 1 to
127 of 134 are 80.31 pct identical
to residues 3 to 128 of 134 from
GenPept : >gb|AAL22216.1|
(AE008854) putative periplasmic
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83730.1"
/db-xref="GI:21956803"
/translation="MTWEYALIGLVGVGVGAVA
MRFGNRKLQQQVLQNELEKSKTD
LEEYRQELVGHFARSALLDNMARDYRQLYQHMA
KSSNNLLPDLPQDNPFYRLTES
EADNDQAPVKLPPRDYSEGASGLLRPEHQNRD"
gene      147907..148311
CDS       147907..148311

/locus-tag="degQ"
/locus-tag="y0137"

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CDS	148564..149955	<pre> /gene="degQ" /locus-tag="y0137" /function="enzyme; degradation of proteins, peptides, glyco" /note="residues 7 to 463 of 463 are 72.05 pct identical to residues 1 to 455 of 455 from E. coli K12 : B3234; residues 7 to 463 of 463 are 72.92 pct identical to residues 1 to 455 of 455 from GenPept : &gt;gb AAL22217.1  (AE008854) serine endoprotease [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="serine endoprotease" /protein-id="AAM83731.1" /db-xref="GI:21956804" /translation="MREFKSMKKTSLLSALAI S VGLGLASVPMVSAALPAAVAGQT LPSLAPMLEKVLPAVVSVHVSQSQAQQORLEEF KFFFGPNAPSGKESRPFEGLGSG VIINAEGYILTNHVINNADKIRVQLNDGREYD AKLLGRDEQTDIALQLTDAKNLT AIKIADSDNLRVGDFAVAVGNPFGLGQTATSGII SALGRSGLNLEGLNFQITDASIN RGNSSGALVNLDELIGINTAILPAGGGNIGIGF AIPSNMAQNLSQQLIEFGEVKRGL LGIRGSEMTADIAKAFNIDAQRGAFVSEVLPKSA AAKAGIKPGDVLISVDGKKISSFA ELRAKVGTTGPGKTIKIGLLREGKPLEVSVTLDN SSSTSTSAENLSPSLQASLSNGE LKDGSKGIKVDVSTKGSFAAQSGLQKDDVIIAVN RERVKDIAELRKAIEAKPAVIALN IVRGEDNIYLLIR" /note="insertion element" </pre>
repeat-region	complement(149966..150675)	/insertion-seq="IS1541a"
gene	complement(150072..150581)	/locus-tag="y0138"
CDS	complement(150072..150581)	<pre> /locus-tag="y0138" /function="IS and transposon related functions" /note="IS1541a; residues 1 to 169 of 169 are 99.40 pct identical to residues 1 to 169 of 169 from GenPept : &gt;gb AAC82673.1  (AF074611) transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83732.1" /db-xref="GI:21956805" /translation="MRSGNCKCSTRNQKGVPMRD EKSLAHTRWNCKYHIVFAPKYRRQ VFYREKKRAIGSILRKLCEWKNVNILEAECCVDH IHMLLEIPPKMSVSGFMGYLKGKS SLMLYEQFGDLKFKYRNREFWCRGYIVDVTGKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK" </pre>

gene	150756..151844	/gene="degS"
CDS	150756..151844	/locus-tag="y0139"
		/gene="degS"
		/locus-tag="y0139"
		/function="enzyme; degradation of proteins, peptides, glyco"
		/note="residues 1 to 349 of 362 are 71.22 pct identical to residues 1 to 350 of 355 from E. coli K12 : B3235"
		/codon-start=1
		/transl-table=11
		/product="protease"
		/protein-id="AAM83733.1"
		/db-xref="GI:21956806"
		/translation="MFLKLLRSIILGLIVAGILL VALPMLRSPGYLFSGKSNVNEEV PTSYNQAVRRAPAVVNVYNRSLSATQQGLAIRT LGSGVIMSDKGYILTNGHVIDAE QIIIVAMQNGRISEALLVGSNDLTLAVLKIDATN LPVIPININRTPHIGDVVLAIGNP YNLGQTVTQGIISATGRIGLSSSGRQNFQITDAS INQSGGALVNTLGLMGMINTLS FDKSNNGETPEGIGFAIPTALATKVMELKIRDGR VIRGYIGITGEEYPPFNANDNGSD RVHGIKVKKVPDGFAPAAQAGIHVGDIIILNVNKP ATSVIETMDQVAEVRPGTTIPVLL LRNGQQIAIVQITITELDQNEMLTTQAAD"
gene	complement(152025..1532 87)	/gene="muraA"
		/locus-tag="y0140"
CDS	complement(152025..1532 87)	/gene="muraA"
		/locus-tag="y0140"
		/function="enzyme; murein sacculus, peptidoglycan"
		/note="first step in murein biosynthesis; residues 1 to 420 of 420 are 88.80 pct identical to residues 1 to 419 of 419 from E. coli K12 : B3189; residues 1 to 420 of 420 are 100.00 pct identical to residues 1 to 420 of 420 from GenPept : >emb CAC92798.1  (AJ414157) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis]"
		/codon-start=1
		/transl-table=11
		/product="UDP-N-glucosamine 1-carboxyvinyltransferase"
		/protein-id="AAM83734.1"
		/db-xref="GI:21956807"
		/translation="MDKFRVQGRTRLSEVTIISG AKNAALPILFAALLAEEPVELQNV PKLKDIDTTIKLLSQLGKTIERNNGSVFVDASAV NEFCAPYDLVKTMRSIHWALGPLV ARFGQGVSLPGGCAIGARPVDLHITGLEQLGAE IKLEEGYVKASVNGRLKAHVMD KVSVGATVTIMSAATLAEGTTVIENAAPEPEIVD TANFLNTLGAKISGAGTDRITIEG"

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VTRLGGGVYRVLPDRIETGTLVAAAISGGKVVC
RQTRPDTLDAVLAKLREAGADIEV
GDDWISLDMQGGKRPKAITFRTAPHGPFPTDMQQAQ
FSLNLNVAEGTGVITETIFENRFM
HVPELIRMGAAHAEIESNTVICYGVQQLSGAQVMA
TDLRASASLVLAGGCIABGVITVDR
IYHIDRGYERIEDKLRLAGAKIERVKGE"
gene      complement(153441..1537 /locus-tag="y0141"
04)
CDS        complement(153441..1537 /locus-tag="y0141"
04)

/notes="residues 4 to 87 of 87 are
80.95 pct identical to residues 6
to 89 of 89 from E. coli K12 :
B3190; residues 4 to 87 of 87 are
80.95 pct identical to residues 6
to 89 of 89 from GenPept :
>gb|AAG58324.1|AE005547-10
(AE005547) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83735.1"
/db-xref="GI:21956808"
/translation="MNLMDTNEIKDVLMLNALAQ
EAHVTGDGSHFQVIVVGELFADMN
RVKKQQAVYAPLMEYIADNRIHALSIKAYTPQEW
QRDRKLNLF"
gene      complement(153842..1541 /locus-tag="y0142"
44)
CDS        complement(153842..1541 /locus-tag="y0142"
44)

/notes="residues 1 to 90 of 100 are
43.33 pct identical to residues 33
to 122 of 129 from E. coli K12 :
B3191; residues 1 to 90 of 100 are
43.33 pct identical to residues 33
to 122 of 129 from GenPept :
>gb|AAG58325.1|AE005547-11
(AE005547) yrbB gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83736.1"
/db-xref="GI:21956809"
/translation="MAGELSWQSLQETLVLQGEI
DRETLPLWQQRETLLADKSRIDV
SQLQRVDSGLALLVHFRELQSQRGHSLEIIGIS
NRLATLIELYNLQIIPVETAS"
gene      complement(154180..1548 /locus-tag="y0143"
03)
CDS        complement(154180..1548 /locus-tag="y0143"
03)

/notes="residues 1 to 207 of 207
are 77.51 pct identical to
residues 1 to 209 of 211 from E.
coli K12 : B3192; residues 1 to
207 of 207 are 77.51 pct identical
to residues 1 to 209 of 211 from

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GenPept : >gb|AAL22179.1|  
 (AE008852) putative ABC  
 superfamily (atp and memb),  
 transport protein [Salmonella  
 typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
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 /protein-id="AAM83737.1"  
 /db-xref="GI:21956810"  
 /translation="MFKRLFMVALLAIAPLVHAV  
 DQSNPYRLMDEAAKKTFTRLKNEQ  
 PKIKQNPFDYLRTIVREELLFPFVQIKYAGALVLS  
 YYKDATPAQREAYFNAPGKYLEQA  
 YGQALALYHGQTYDVAPDQPLGDANIVAIRVTIL  
 DFGSRPPVRLDFQWRKNSQTGNWQ  
 AYDMIAEGVSMISTKQNEWASILRQKGV DGLTQQ  
 LLSAAKQPIITLTK"  
 /locus-tag="y0144"

gene complement(154816..1553  
 88)  
 CDS complement(154816..1553  
 88)

/note="residues 6 to 178 of 190  
 are 71.67 pct identical to  
 residues 1 to 170 of 183 from E.  
 coli K12 : B3193; residues 6 to  
 184 of 190 are 67.59 pct identical  
 to residues 1 to 179 of 183 from  
 GenPept : >gb|AAL22180.1|  
 (AE008852) putative ABC  
 superfamily (bind-prot) transport  
 protein [Salmonella typhimurium  
 LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical protein"  
 /protein-id="AAM83738.1"  
 /db-xref="GI:21956811"  
 /translation="MGTESMQTKKSEVWVGMFIL  
 IAILAVIFLCLKVADIKSVGNQPT  
 YRIYANFDNIGGLKNHSPVKIGGVVGRVAEITL  
 DTKNYPTRVAIDIQQRYNHIDPTS  
 SLAVRTSGLLGEEFLALNVGFEDPEMGTSILKDG  
 GTIQDTKSALVLEDLIGQFLYKSS  
 GDSPAVSETAPATETAAFPQAAVPSLPAQHP"  
 /locus-tag="y0145"

gene complement(155378..1561  
 60)  
 CDS complement(155378..1561  
 60)

/note="residues 1 to 260 of 260  
 are 82.69 pct identical to  
 residues 1 to 260 of 260 from E.  
 coli K12 : B3194"  
 /codon-start=1  
 /transl-table=11  
 /product="hypothetical protein"  
 /protein-id="AAM83739.1"  
 /db-xref="GI:21956812"  
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 GRAGLMLFNLVGRPEPRKQWPLL  
 IKQLYSVGVQSLLIIVVSGLFIGMVLGLQGFLIL  
 TTYSAEASLGMMVSLSLRELGPV"

VTALLFAGRAGSALTAEIGLMKATEQISSLEMMMA  
IDPLRRVVAPRFWAGLISMPLLTA  
IFVAVGWGGSVVGVWDWKGIDSGFFWSAMQNAVE  
WRTDLLNCLIKSLVFALTVTWIAL  
FNGYDAVPTSEGISRATTRTVVHSSLAVALGLDFV  
LTALMFGN"

gene complement(156378..1571 /locus-tag="y0146"  
96)

CDS complement(156378..1571 /locus-tag="y0146"  
96)

/function="putative transport"  
/note="residues 4 to 269 of 272  
are 78.19 pct identical to  
residues 1 to 266 of 269 from E.  
coli K12 : B3195"  
/codon-start=1  
/transl-table=11  
/product="putative ATP-binding  
component of ABC transport system"  
/protein-id="AAM83740.1"  
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RGERLIFADINMTVPRGKVTAIMG  
PSGIGKTTLLRLIGGQLAPDTGEIWFEDGNIPAL  
SRQRLYDVRKKMSMLFQSGALFTD  
LTVFENVAFPLREHSRLPEELLHSTVMMKLEAVG  
LRGAANLMPAELSGGMARRAALAR  
AIALDPPELIMFDEPFVGGDPITMGVLVKLIDELN  
HALGVTCVVVSHDVEVLSTADYA  
YIVADQHVIAEGTPEQLQTNDSMRVRQFLDGIAD  
GPVFFRFPAAGDYKTELLYPK"

gene 157461..158435  
CDS 157461..158435

/locus-tag="y0147"  
/locus-tag="y0147"  
/note="residues 1 to 318 of 324  
are 60.69 pct identical to  
residues 1 to 318 of 325 from E.  
coli K12 : B3196; residues 1 to  
318 of 324 are 63.52 pct identical  
to residues 1 to 318 of 325 from  
GenPept : >emb|CAD07831.1|  
(AL627278) putative membrane  
protein [Salmonella enterica  
subsp. enterica serovar Typhi]"  
/codon-start=1  
/transl-table=11  
/product="hypothetical protein"  
/protein-id="AAM83741.1"  
/db-xref="GI:21956815"  
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TNLLLIIVGGAALIRPLIVRSEILR  
RELPLMLVVTALCGFLLADNHLSRGDGVILLAA  
AAFIVLMLKIARLAHAEGNDILTR  
EQLSELFPQDSSTTVALWLVLAFIILPLSAKMII  
DNATVIARVAGVSELVIGLTVIAI  
GTSLPELATFIAAGALKGENDIAVGNIIGSNIFNI  
VIVLGPVALLSPGEINPEAFQORDY  
WVMLAVSVVFTLLCLRKHRIHLAGALLCGFI  
TYLAVLFFAPISAL"

gene 158459..159532  
CDS 158459..159532 /locus-tag="y0149"  
/locus-tag="y0149"



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/note="residues 30 to 357 of 357
are 77.43 pct identical to
residues 1 to 328 of 328 from E.
coli K12 : B3197; residues 30 to
357 of 357 are 78.65 pct identical
to residues 1 to 328 of 328 from
GenPept : >gb|AAL22184.1|
(AE008852) putative polysialic
acid capsule expression protein
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="putative isomerase"
/protein-id="AAM83742.1"
/db-xref="GI:21956816"
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GKVVMGMGKSGHIGCKIAATFAS
TGTPAFFVHPGEASHGDLGMITPDQDIVLAISNSG
ESNEILTLPVPLKRQKILLICMSS
NPESTMGKAADIHLCINVPQEAACPLGLAPTITST
ATLVMGDALAVALLKARGFTQEDF
ALSHPGGALGRKLLRLSDDIMHTGTEIPTVSPDA
SLRDALLEITRKSGLTIVICDDSM
RIKGIFTDGDLLRRVDFMDGIDLNNAKIADVMTRGG
IRVPPNILAVDALNLMESRHITAL
LVADGDQLLGVVHMDMLRAGVV"
locus-tag="y0148"

gene      complement(159121..1594
08)
CDS       complement(159121..1594
08)

/note="residues 18 to 78 of 95 are
32.78 pct identical to residues
645 to 704 of 918 from GenPept :
>gb|AAA33114.1| (M33154) nitrate
reductase [Cucurbita maxima]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83743.1"
/db-xref="GI:21956817"
/translation="MFGGTRIPPRVMTSAIFALF
RSMPISNTRRKSFSVKIPLILIES
SQITVKPRLFRVISSKASRNDASGLTVGISVPC
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/locus-tag="y0150"
/locus-tag="y0150"
/note="residues 5 to 187 of 187
are 77.04 pct identical to
residues 6 to 188 of 188 from E.
coli K12 : B3198"
/codon-start=1
/transl-table=11
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/protein-id="AAM83744.1"
/db-xref="GI:21956818"
/translation="MSNTAYITDCYGPVADDVIQ
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NQGEELKAFNVRDGYGIRCLITSDDIVAITGRR
AKLLEDNANTLGITHLYQGQSDKL
VAYHELLATLQCQPEQVAYIGDDLIDWPVMAQVG

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gene 160341..160904  
CDS 160341..160904

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GRGAVREVCDLILLAQDKLEGATGLSI"
/locus-tag="y0151"
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/note="residues 1 to 186 of 187
are 55.91 pct identical to
residues 1 to 185 of 191 from E.
coli K12 : B3199"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83745.1"
/db-xref="GI:21956819"
/translation="MSKTRRWITLVLALIALALI
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FTKPVMTLFGDNAVATWTVRADRA
KLTDKMLYLYGHVEVDSLTAQAQLKKIRTDNAQ
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/locus-tag="y0152"
/locus-tag="y0152"
/note="residues 8 to 177 of 188
are 69.76 pct identical to
residues 1 to 172 of 185 from E.
coli K12 : B3200; residues 8 to
187 of 188 are 69.94 pct identical
to residues 1 to 183 of 184 from
GenPept : >gb|AAL22187.1|
(AE008852) putative ABC
superfamily (bind-prot) transport
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83746.1"
/db-xref="GI:21956820"
/translation="MKRLKPLMKSKNKISHLLLA
CSLLAASLSAFALTGDTQPAEVK
SDKQTLDMETNTVTFIDNVVIKQGTIEIKADKVV
VTRPGGDQSKMIIIEGFGNPVTFYQ
MQDSGKFPVKHGQKRLRYEIANDFVLTGDAYLEQ
LDSNIKGDRITYLVKKQQMEAFSD
KGRKRVTTVLLPSQLQDKGPAASGQKKSK"
/locus-tag="y0153"
/locus-tag="y0153"
/function="putative transport"
/note="residues 1 to 241 of 241
are 88.79 pct identical to
residues 1 to 241 of 241 from E.
coli K12 : B3201; residues 1 to
241 of 241 are 88.79 pct identical
to residues 1 to 241 of 241 from
GenPept : >gb|AAL22188.1|
(AE008852) putative ABC
superfamily (atp-bind) transport
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
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gene 160867..161433  
CDS 160867..161433

gene 161440..162165  
CDS 161440..162165

		component of ABC transport system"
		/protein-id="AAM83747.1"
		/db-xref="GI:21956821"
		/translation="MATLIAEKLAKAYKGRKVVE
		DVSLNVKSGEIVLLGPNAGKTT
		TFYMVVGIVQRDAGRIVDEDDISLLPLHERARR
		GIGYLPQEAISIFRRLSVFNLMMAV
		LEIRKDLSAEQREERAEEELMEEFHNHLRDSLQ
		SLSGGERRRVEIARALANPKFIL
		LDEPFAGVDPISVIDIKKIIKHLRDSGLGLVITD
		HNVRETLDVCERAYIVSQGHILAH
		GTPQDILADEQVKRVYLGEEFRL"
gene	162227..163660	/gene="rpoN"
		/locus-tag="y0154"
CDS	162227..163660	/gene="rpoN"
		/locus-tag="y0154"
		/function="regulator; global
		regulatory functions"
		/note="nitrogen and fermentation
		regulation; residues 1 to 477 of
		477 are 82.59 pct identical to
		residues 1 to 477 of 477 from E.
		coli K12 : B3202; residues 1 to
		477 of 477 are 82.38 pct identical
		to residues 1 to 477 of 477 from
		GenPept : >emb CAA26925.1
		(X03147) ntrA protein (aa 1-477)
		[Klebsiella pneumoniae]"
		/codon-start=1
		/transl-table=11
		/product="RNA polymerase, sigma(54
		or 60) factor"
		/protein-id="AAM83748.1"
		/db-xref="GI:21956822"
		/translation="MKQGLQLKFSQQLAMTPQLQ
		QAIRLLQLSTLELQEEIQLALESN
		PLLEQTDLHEEIDAKETVDSESLDTREALEQKDM
		PEELPLDATWDEIYTAGTPSGMGN
		DYSDELVPYQGETTQTLQDYLMWQVDLTPFTET
		DAAIATSIIVDAVDDTGYLTVPLED
		ILESMDGENVALDEVAVLKRIQHFDPIGVAARN
		LRECLLVQLSQYAKDTPYLAEARL
		IVSEYLDLLGNHDFRMMIRLSRLKEDTLKEAIAL
		IQSLDPRPGQSINTGESEYVIPDV
		LVRKEKGIWTVELNADSIPLKVMNQYAAMGNSV
		RNDSDGQFIRSNLQEAKWIKSLE
		SRNETLLKVARCIVEQQVEFFEKGAEFMKPMVLA
		DIAQAVDMHESTISRVTQKFLHS
		PRGIFELKYFFSSHVNTDSGGEASSTAIRALVKK
		LVAENPAKPLSDSKLTLLCEQG
		IMVARRTVAKYRESLSIPPSNQKQLV"
		/locus-tag="y0155"
gene	163684..163791	/locus-tag="y0155"
CDS	163684..163791	/function="putative regulator;
		global regulatory functions"
		/note="residues 1 to 35 of 35 are
		94.28 pct identical to residues 1
		to 35 of 95 from GenPept :
		>gb AAL22190.1  (AE008852)
		putative sigma N modulation factor
		[Salmonella typhimurium LT2]"
		/codon-start=1

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/translation="MQLNITGHHVEITEALREFV
TKKFAKLEQYFDRIN"
/locus-tag="y0156"
/locus-tag="y0156"
/function="putative regulator;
global regulatory functions"
/notes="residues 1 to 57 of 57 are
73.68 pct identical to residues 39
to 95 of 95 from E. coli K12 :
B3203; residues 1 to 57 of 57 are
77.19 pct identical to residues 39
to 95 of 95 from GenPept :
>emb|CAA34391.1| (X16335) ORF95
peptide (AA 1-95) [Klebsiella
pneumoniae]"
/codon-start=1
/transl-table=11
/product="probable sigma-54
modulation protein"
/protein-id="AAM83750.1"
/db-xref="GI:21956824"
/translation="MVLSEKVKQIAEATVHVNG
GELHASSEQEDMYAAIDILVDKLA
RQLNKHKKDLKKQH"
/gene="ptsN"
/locus-tag="y0157"
/gene="ptsN"
/locus-tag="y0157"
/function="enzyme; transport of
small molecules; amino acids,
amines"
/notes="regulates N metabolism;
residues 7 to 158 of 164 are 86.18
pct identical to residues 4 to 155
of 163 from E. coli K12 : B3204;
residues 7 to 158 of 164 are 86.18
pct identical to residues 4 to 155
of 163 from GenPept :
>gb|AAG58338.1|AE005548-9
(AE005548) phosphotransferase
system enzyme IIA, regulates N
metabolism [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="phosphotransferase
system enzyme IIA"
/protein-id="AAM83751.1"
/db-xref="GI:21956825"
/translation="MKDEMTNDPALQLSSVLNIE
STKSSVHCSSKKRALEIISLAAK
QLNLPSQVVFDAVLTRRMGSTGIGSGIAIPHGK
LEEDTLRAVGVFIRLEQPIAFDAI
DNQPVDLLFALLVPADQCKTHLHTLSLVAKRLAD
KTVCRRLRSQAQSDDELYQIITELP PEIA"
/locus-tag="y0158"
/locus-tag="y0158"

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gene	163798..163971
CDS	163798..163971
gene	164077..164571
CDS	164077..164571
gene	164877..165731
CDS	164877..165731

```

/note="residues 1 to 283 of 284
are 94.34 pct identical to
residues 1 to 283 of 284 from E.
coli K12 : B3205"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83752.1"
/db-xref="GI:21956826"
/translation="MVLMIIVSGRSGSGKSVLR
LEDMGFYCVDNLFVVLLPQLASTL
ADRNISAAVSIDVRNMPESPEVFEHAMTQLPDSF
SPQLFLDADRNTLIRRYSDTRRL
HPLSAKNLSLESAIDESDLLEPLRSRADLIIDT
SEMSVHELAEMLRTRLGKREREL
TMVFESFGFKHGIPIDADYVDFVRFLPNPHWDPK
LRPMTGLDKFVISFLDRHTEVHNF
IYQTRSYLEQWLPMLETNNSYLTVAIGCTGGKH
RSVYVAEQLDADYFRARGKNVQSRH RTLEKRKQ"
gene      165728..166000 /gene="ptsO"
CDS        165728..166000 /locus-tag="y0159"
           /gene="ptsO"
           /locus-tag="y0159"
           /function="transport; transport of
           small molecules; Other"
           /note="nitrogen related, exchanges
           phosphate with Enzyme I, Hpr;
           residues 1 to 90 of 90 are 87.77
           pct identical to residues 1 to 90
           of 90 from E. coli K12 : B3206;
           residues 1 to 90 of 90 are 85.55
           pct identical to residues 1 to 90
           of 90 from GenPept :
           >gb|AAL22193.1| (AE008853) NPr,
           phosphocarrier protein HPr-like
           NPr, nitrogen related, exchanges
           phosphate with Enzyme I
           [Salmonella typhimurium LT2]"
           /codon-start=1
           /transl-table=11
           /product="phosphocarrier protein
           HPr-like NPr"
           /protein-id="AAM83753.1"
           /db-xref="GI:21956827"
           /translation="MTVKQTVEIKNKLGMHARPA
           MKLFELVQSFDAEVMLRNDSGTEA
           EASSVIALMLDSAKGRQIEVEATGVDEIQALAA
           VIELFNSGFDED"
gene      complement(165896..1661 /locus-tag="y0160"
47)
CDS        complement(165896..1661 /locus-tag="y0160"
47)
           /codon-start=1
           /transl-table=11
           /product="hypothetical"
           /protein-id="AAM83754.1"
           /db-xref="GI:21956828"
           /translation="MHVVQONIGGFSSFPFANCG
           ELYSRLISLQGVKIVFFVLSKRLP
           TLRAPLIFVKSRIKQLDNRCQCLNFINPGCFNLY
           LAAFG"
gene      166338..167273 /gene="pyrB"

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CDS	166338..167273	<pre> /locus-tag="y0161" /gene="pyrB" /locus-tag="y0161" /function="enzyme; pyrimidine ribonucleotide biosynthesis" /note="residues 1 to 311 of 311 are 84.88 pct identical to residues 1 to 311 of 311 from E. coli K12 : B4245; residues 1 to 311 of 311 are 85.85 pct identical to residues 1 to 311 of 311 from GenPept : &gt;gb AAL23279.1  (AE008909) aspartate carbamoyltransferase, catalytic subunit [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="aspartate carbamoyltransferase, catalytic subunit" /protein-id="AAM83755.1" /db-xref="GI:21956830" /translation="MANPLYHKHIISINDLSRDE LELVLRITASLKKTFPELLKHKV IASCFEASIRTRLSFETSIHRLGASVVGFSDDSS NTSLGKKGETLADIMSVISTYVDA IVMRHPQEGASRLAAQFSGNVPIVNAAGDGANQHP TQTLLDLFTIQETQGRLDNINIAM VGDLKYGRITVHSLTQALAKFNGNHFFFIAPDALA MPAYILQMLEEKEIEYSLHESLEE VVPELDILYMTRVOKERLDPSEYANVKAQFILRS SDLTGARDNLKVLHPLPRIDEITT DVDKTPYAYYFQQAGNGIFARQALLVLNAELA L" </pre>
gene	167279..167749	<pre> /gene="pyrI" </pre>
CDS	167279..167749	<pre> /locus-tag="y0162" /gene="pyrI" /locus-tag="y0162" /function="enzyme; pyrimidine ribonucleotide biosynthesis" /note="residues 3 to 153 of 156 are 78.80 pct identical to residues 1 to 151 of 153 from E. coli K12 : B4244; residues 3 to 156 of 156 are 83.11 pct identical to residues 1 to 154 of 154 from GenPept : &gt;gb AAA26565.1  (J05033) aspartate transcarbamoylase [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="aspartate carbamoyltransferase, regulatory subunit" /protein-id="AAM83756.1" /db-xref="GI:21956831" /translation="MMMTQDYKLQVEAIKCGTVI DHIPAQIGFKLLSLFKLTATDQRI TIGLNLPSKRSGRKDLIKIENTFLTEQQANQLAM YAPDATVNRIDNYEVVKLTLSTLP ERIDAVLTCPNSNCISHNEPVDSSFTVKAQRGEI </pre>

gene	167848..168273	SLKCKYCEKEFDHLTLVLHAD"
CDS	167848..168273	/locus-tag="y0163" /locus-tag="y0163" /note="residues 11 to 141 of 141 are 83.20 pct identical to residues 11 to 141 of 141 from E. coli K12 : B4243; residues 14 to 141 of 141 are 85.93 pct identical to residues 1 to 128 of 128 from GenPept : >gb AAL23277.1  (AE008909) putative translation initiation inhibitor [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83757.1" /db-xref="GI:21956832" /translation="MISLSALRKSGVKMLRAIKT KLAPAAIGPYVQGVDLGSMIMTSG QIPIDPKTGLVADDIAAQAQSQLENVKAIVEAAG LKVADIVKTTVFVKDLNDFSIVNA TYEAFFTEHSAPFFPARSCVEVARLPKDVKIEIEA IAVRR" /locus-tag="y0164" /locus-tag="y0164" /note="residues 62 to 143 of 158 are 31.70 pct identical to residues 1565 to 1640 of 3016 from GenPept : >dbj BAA17634.1  (D90907) ORF-ID:slr1403 integrin alpha- and beta4- subunit domain homolog [Synechocystis sp. PCC 6803]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83758.1" /db-xref="GI:21956833" /translation="MKLRTWLLIPIICSPFFWGS TAIAKNGVAIPLPDKRVAVLSEGD LESASVGTYSVAIFKNDTFLDFIAGGVFSRDSGI FQDNGKPRVEFTDINGDGNKELIV SQLTAGSGNYLRVDAFSLGPDSSINKVLSIQSDTK SDYISLLKELCEICLPIDAPPH" /gene="treR" /locus-tag="y0165" /gene="treR" /locus-tag="y0165" /function="regulator; osmotic adaptation" /note="residues 1 to 316 of 317 are 62.02 pct identical to residues 1 to 314 of 315 from E. coli K12 : B4241; residues 1 to 316 of 317 are 62.02 pct identical to residues 1 to 314 of 315 from GenPept : >dbj BAB38641.1  (AP002568) repressor of treA,B,C [Escherichia coli O157:H7]" /codon-start=1 /transl-table=11
gene	168572..169048	
CDS	168572..169048	
gene	169282..170235	
CDS	169282..170235	

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/product="repressor of treA,B,C"
/protein-id="AAM83759.1"
/db-xref="GI:21956834"
/translation="MQNRLTIKDIARMSGVGKST
VSRVLNNEGSVSPQTRERVEAVIR
QHGFTPSKSARAMRGQSDKVVGIIVSRLDSPSEN
QAVRTMLPLFYQQGYDPILMESQF
DTILVSEHLHILQQRHVDGVILFGFSGLTAEMLA
FWQEKMMVVLAREYRGFSSVCYDDE
GAIYLLMDKLRQAGHRHISYIGVQSSDATTGMRR
YQAYLDYSQQHGLTPMVALGELSY
QSGFQLAPQVITPQTSALVCASDTIAMGVSKYLQ
QQEREQPPIQVCGIGNTPLHLFLF
PDTLTIELGYGRAGVKAAQQLLDQLSNSQPIQI
IIPGQLV"
/gene="treB"
/locus-tag="y0166"
CDS 170610..172061
/gene="treB"
/locus-tag="y0166"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="trehalose specific;
residues 13 to 483 of 483 are
80.46 pct identical to residues 2
to 472 of 473 from E. coli K12 :
B4240; residues 13 to 483 of 483
are 80.89 pct identical to
residues 2 to 472 of 473 from
GenPept : >dbj|BAB38640.1|
(AP002568) trehalose specific PTS
system enzyme II [Escherichia coli
O157:H7]"
/codon-start=1
/transl-table=11
/product="PTS system enzyme IIBC"
/protein-id="AAM83760.1"
/db-xref="GI:21956835"
/translation="MRARNLYGKDDKMGKVKKQD
IDQLIVLVGGRENIATVSHCITRL
RFVLKDPASIASPKEIENLSMVKGCFNAGQFQVY
IGPEVDDYYKALIAKIQSEVDKE
QTKLAARQNMTHFERGISHFAEIFFPLLPALISG
GLILGFRNVIGDIPMSEGKTLAQM
YPAWQTIYDFLWLLGEAIFFFLPVAICWSTVKKM
GGTPVLGIVLGITLVSPQLMNSYL
LGQQLPDVWNFGWFTIEKVGYQAQVIPSILAGLA
LGWIETNLKRIIPAYLYLVVVPV
SLLLVFLAHTLIGPFGRMIGDGVANGVKAVMTG
SFAPVGAALFGFLYAPLVITGVHQ
TTLAIDMQMVQSMGGTPVWPLIALNSIAQASAVL
GIIISRKINEREISVPAAISAYL
GVTEPAMYGINLKRYRFPMLCAMILGALICGL
TGVNANGIGVGGLPGLISIQPFW
GIYAVAMLVAVIIVPLALTIILVYKRKRERGELPV"
gene 172156..173823
/gene="treC"
/locus-tag="y0167"
CDS 172156..173823
/gene="treC"
/locus-tag="y0167"
/function="enzyme; degradation of
small molecules; Carbon compounds"
/note="residues 7 to 553 of 555"

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are 73.85 pct identical to  
residues 7 to 549 of 551 from E.  
coli K12 : B4239; residues 7 to  
553 of 555 are 73.12 pct identical  
to residues 6 to 548 of 550 from  
GenPept : >emb|CAD06914.1|  
(AL627283) trehalose-6-phosphate  
hydrolase [Salmonella enterica  
subsp. enterica serovar Typhij]  
/codon-start=1  
/transl-table=11  
/product="trehalase 6-P hydrolase"  
/protein-id="AAM83761.1"  
/db-xref="GI:21956836"  
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FQDSTGNGYGDLAGVAQRLDYLOK  
LGVDIAIWLIPVYVSPQVDNGYDVADYCAIDPAYG  
TLDDFKRLVAGAHQRGIRIIMDMV  
FNHTSTEAWFKASQDRNSPYRQFYIWRDGDGGD  
GSLPNNWRSKFGGHAQQWHAASGQ  
YYLHLFAPEQADLNWEHQPVVRDELKKVCEFWADL  
GVDGLRLDVINLVSKQQDFPNLDL  
GDGRRFYTDGPRIHEFLQELSRDVFQPRRLMTVG  
EMSSTRLEHCQRYAALGGDELSMT  
FNFHHLKVVDYLNGEKLMLPFPNRVELKHIFNQWQ  
QGMHNRANWALFWCNHDQPRIVSR  
FGHEGALRLPAAKMLAMVLHGMQGTPIYIQGEEI  
GMTNPNTDITQYRDVESLNMFAE  
LSVAGREPDDELLAILAASRDNSRTPMQWDSND  
AGFSQGTPIWAPCSNYHEINVNA  
LADADSVFYAYQYLIALRKQYDIFTFGDYQDLCP  
QHPDLWCYLRSWQGLLVVANLS  
EEPQRWQPEGLTLDGNWQLMSSYDQSAFQPQDM  
ILRGYEGIIYWVCE"  
/gene="rnk"  
/locus-tag="y0168"  
/gene="rnk"  
/locus-tag="y0168"  
/function="regulator; central  
intermediary metabolism:  
Nucleotide interconversions"  
/note="residues 1 to 134 of 136  
are 64.92 pct identical to  
residues 1 to 134 of 136 from E.  
coli K12 : B0610"  
/codon-start=1  
/transl-table=11  
/product="regulator of nucleoside  
diphosphate kinase"  
/protein-id="AAM83762.1"  
/db-xref="GI:21956837"  
/translation="MTKPTTITINELDAERLDALL  
AQPFAAGSVVATALNEELDRAEIL  
PPNEIPADVVTMNSRVRLDLNSQEEHIRTIVYP  
ASLKDSEQLSVMAPLGAALLGLH  
VNDEISWKLPGGDETRITVLELLYQPESAGEYHR  
"

gene 174176..174586

CDS 174176..174586

gene complement(174818..1752  
10) /gene="cybC"

/locus-tag="y0169"

CDS complement(174818..1752  
10) /gene="cybC"

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/locus-tag="y0169"
/function="enzyme; energy
metabolism, carbon: Electron
transport"
/note="residues 31 to 130 of 130
are 57.99 pct identical to
residues 1 to 100 of 100 from E.
coli K12 : B4236; residues 3 to
130 of 130 are 52.34 pct identical
to residues 1 to 128 of 128 from
GenPept : >gb|AAL23259.1|
(AE008908) cytochrome b(562)
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="cytochrome b(562)"
/protein-id="AAM83763.1"
/db-xref="GI:21956838"
/translation="MSMGKTLMALITAALLSTSS
LVMAASVADDMETIAEHYGVKLA
DSTAVIKQDLQAMRVAAVDAQGIPTKLKSKVED
SPENKDFRHGMDVLIGEIDGALAL
ADQGLDEAKQAQDFKDTRTYHKKYR"
gene      complement(175412..1760 /locus-tag="y0170"
56)
CDS       complement(175412..1760 /locus-tag="y0170"
56)

/note="residues 25 to 134 of 214
are 23.21 pct identical to
residues 51 to 159 of 320 from
GenPept : >gb|AAC06973.1|
(AE000710) pyridoxal phosphate
biosynthetic protein PdxA [Aquifex
aeolicus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83764.1"
/db-xref="GI:21956839"
/translation="MIMFVLIRGSSNMIVMPSTY
SPATIAREFKVIHEFELSSMKYGV
IFDKNVPEKAAIIRMNTESFNGIPRHRRII AALDLV
AKQELGENVISVQRFWQDSALFQV
EGMVVEQGARGKGLATLLYEELVVKCGVILMSDN
KQYEAGKALWQKIAQESDKLAVFI
LDSVDVGQFYPCGDRVPYNGKGIPEEKIWSLHPD
TTKWGVVLVAENREKISQYC"
gene      complement(176305..1776 /gene="pmbA"
45)
CDS       complement(176305..1776 /locus-tag="y0171"
45) /gene="pmbA"

/locus-tag="y0171"
/function="phenotype; proteins -
translation and modification"
/note="maturation of antibiotic
MccB17, see tld genes; residues 1
to 446 of 446 are 82.73 pct
identical to residues 5 to 450 of
450 from E. coli K12 : B4235"
/codon-start=1
/transl-table=11

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		<pre> /product="PmbA/TldD family protein" /protein-id="AAM83765.1" /db-xref="GI:21956841" /translation="MKVVTQVAEQRKLTLEQAVAQ ALELARVGSDDAAEAVASKTTGISV STRFGEVENVFNSDGDALGITVYHQQRKGSASTT DLNPDAVARTVQAALDIARTYSPD FYAGPADKSLFLADAPDLDFHFGDLDAAEQGILL AARAEQAALQADKRITNTEGGSFN SHYGKVFVGNHGLQSYCSSRHSLSSSVIAEHN GDMERDYATTIGRRMEDLATPEWV GEECARTLSRLSPRKLPMTQSPVLFAAEVATGL FGHLVSAISGGNIYRKSTFLLDHL GQQLPEWLTIEEHPHLLRGLASTPFDSEGVRTL QREIVKDGVLQTYLLTSYSARKLG LQSTGHAGGIHNWRIAGQGQDFAGMLKQLDKGLV VTELMGGQVSTVTDGYSRGAAGFW VENGEIQYPVSEITTIAGNLKMDLRNIVSVGSDIE TRSNIQCGSVLLPVMKIAQE" /locus-tag="y0172" /locus-tag="y0172" /function="phenotype; Not classified" /notes="residues 3 to 183 of 184 are 78.02 pct identical to residues 1 to 182 of 183 from E. coli K12 : B4234" /codon-start=1 /transl-table=11 /product="putative alpha helix protein" /protein-id="AAM83766.1" /db-xref="GI:21956842" /translation="MTMNKQPEDWLDVDPENKND DDDEIIWVSKSEIKRDAEALKDLG TELVDLGKNALERIPLDEDLLAAIELAQIKKEG RRRQLQLIGKMLRARDVEPIQTAL DKLKNRHNQQISLFHKLETLRDLIAEGDEAIP VLELYPDADRQQLRSLVRNAQKEQ AANKPPKSRQIFSYLRELAKKQ" /locus-tag="y0173" /locus-tag="y0173" /notes="residues 6 to 87 of 93 are 53.01 pct identical to residues 6 to 88 of 90 from E. coli K12 : B3239" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83767.1" /db-xref="GI:21956843" /translation="MKVVVDFNHIPDLPAFYRA FSQNFALSEDFGANLDALWDVVTG EIALPVIEIEVFHFSRRHQRRFAAIVLLLEEAE LAGRLHFNVVDEHIV" /locus-tag="y0174" /locus-tag="y0174" </pre>
gene	177820..178374	
CDS	177820..178374	
gene	complement(178486..178767)	
CDS	complement(178486..178767)	
gene	complement(178772..179245)	
CDS	complement(178772..179245)	

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/function="enzyme; macromolecule
degradation: Degradation of RNA"
/note="residues 1 to 156 of 157
are 47.43 pct identical to
residues 1 to 148 of 149 from
GenPept : >gb|AAA86441.1| (M14442)
barnase (RNase) precursor
[Bacillus amyloliquefaciens]"
/codon-start=1
/transl-table=11
/product="putative ribonuclease"
/protein-id="AAM83768.1"
/db-xref="GI:21956844"
/translation="MNKRLMAILGAVLLLIAGAW
QGIDGVTVRDIGSSAELERPALSA
SAATESLTQHOKVVKYLQTHHRLPDFYLTKKQAR
EQGWDAQGNLDCVLPGKAIGGDR
FSNRERQLPDAKGRHWREADVNYRCGRGRSDRL
YSNDGLIYLTQDHYKHFIRME"
gene      complement(179440..1797 /locus-tag="y0175"
78)
CDS       complement(179440..1797 /locus-tag="y0175"
78)

/note="residues 1 to 112 of 112
are 59.82 pct identical to
residues 374 to 485 of 486 from
GenPept : >gb|AAL44216.1|
(AE009270) succinate semialdehyde
dehydrogenase [Agrobacterium
tumefaciens str. C58 (U.
Washington)]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83769.1"
/db-xref="GI:21956845"
/translation="MIADANEQMKVASEETFGPL
AACFRFSTEAEVIQRANNTFPGLA
AYFYTONLQRVFRVSEALESGMIGVNECSVSTEL
APFGGVKESGLGREGSVLGLDEFM
EVKTLHLGNL"
gene      complement(179775..1809 /gene="gabD"
08)
CDS       complement(179775..1809 /gene="gabD"
08)

/locus-tag="y0176"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="NADP-dependent activity;
residues 23 to 366 of 377 are
56.06 pct identical to residues 15
to 360 of 482 from E. coli K12 :
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dehydrogenase"
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IPSAKEGARILATREPIGVVAIT
PWNFPLAMLTRKLG PALAAGCTGLIKPANNTPLS
AFALLALAEQAGVPAGVLNGVGD
THAISDAIMASSDVRKISFTGSTNVGKTLMRNAA
ATMKRISMELGGNAPYIVFDDADL
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FVNRLAAEVKKLVKGNGMDKDVNM
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gene      complement(181175..1831 /locus-tag="y0177"
30)
CDS       complement(181175..1831 /locus-tag="y0177"
30)

/note="residues 9 to 650 of 651
are 64.64 pct identical to
residues 11 to 652 of 655 from E.
coli K12 : B3240; residues 9 to
650 of 651 are 64.79 pct identical
to residues 11 to 652 of 655 from
GenPept :
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(AE005551) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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67)
CDS       complement(183132..1840 /locus-tag="y0178"
67)

/function="putative membrane"
/note="residues 1 to 311 of 311

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are 72.66 pct identical to  
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coli K12 : B3241; residues 1 to  
311 of 311 are 100.00 pct  
identical to residues 1 to 311 of  
311 from GenPept :  
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putative HlyD family secretion  
protein [Yersinia pestis]"  
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EKQRESSRRHRLGIQALSQEEIDQASNVLTQVQH  
QLAKAIAVRDLARLDLERTTVRAP  
AEGWVTNLNVHAGEFIRNGATAVALVKKDTFYIL  
AYLEETKLEGVKPGYRAEITPLGS  
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EWWRLAQRVFPVKIHLDSQYLY  
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G"

gene complement(184075..1842 /locus-tag="y0179"  
78)

CDS complement(184075..1842 /locus-tag="y0179"  
78)

/note="residues 1 to 66 of 67 are  
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to 89 of 90 from E. coli K12 :  
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/translation="MSLLPVMVIFGLSFPPIFLE  
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gene 184581..185492  
CDS 184581..185492

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/protein-id="AAM83774.1"  
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AAARRLENSVSSISQTVSKLENEL  
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VHEQLYAFNNPTGTGLRIGCSSTM  
AQNVLATMTADMMLKAYPGLSVNLVAGIPAPDLIA  
DGLDVVIRVGALQNSGLFSRRLGA

gene	185744..186619	MPMVVCAAKSYLSQYGTAPAKPSDMANFSWLEYNV RPDSNFELIAPEGITTIQISQGRF VTNDSQTMIRWLKAGAGIAYTPLMWVIEEIKRGE VEILFKHYHSDPRPVYALYTEKDK MPLKVQVCIDYLTLEYFKRVADVYQDYR"
CDS	185744..186619	/locus-tag="y0181" /locus-tag="y0181" /function="regulator" /note="residues 4 to 182 of 291 are 26.76 pct identical to residues 8 to 200 of 303 from GenPept : >gb AAC75958.1  (AE000375) putative transcriptional regulator LYSR-type [Escherichia coli K12]" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="AAM83775.1" /db-xref="GI:21956851" /translation="MVHMFISKNLLVFFTTVQEG SLTNAAVKLFITTTPPMRSRLKILE EELGFKLFRTRTISGLKLTLEGAIFYQEIYPTIVR LTEITKNYKKNKNGIINIATYQLN SDHAGVICDYFIKKGNFNIELRENIGDISQMDIV ISTKEIKGYDFDIETLASCSEIKLL YASHLNDLPDRVEYLKLPFIQSSIFCSCSCCFKR FSHNLIQQGYSGNVLRIIDARVRH EIIKKGAGISLSTNYFFDKKKISHSTEISFISDI NFDITYYIYFKSSVINKEFFIYI TNNSLQWQKAEEKH"
gene	complement(186780..186941)	/locus-tag="y0182"
CDS	complement(186780..186941)	/locus-tag="y0182"  /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83776.1" /db-xref="GI:21956853" /translation="MALFCFGLMNRISIRYNG CSMVDIILHNLPLYLGTLANVDVKQ QVLTMCCLK"
gene	187032..189356	/gene="tcaA1" /locus-tag="y0183"
CDS	187032..189356	/gene="tcaA1" /locus-tag="y0183" /function="putative factor; extracellular functions; secreted proteins" /note="residues 182 to 557 of 774 are 35.41 pct identical to residues 602 to 996 of 1095 from GenPept : >gb AAL18449.1  (AF346497) toxin complex protein [Photorhabdus luminescens]" /codon-start=1 /transl-table=11 /product="putative toxin subunit" /protein-id="AAM83777.1" /db-xref="GI:21956854"

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 IISEYRRLHQRVGLSDVPFIAIINAVNTTHTNEN  
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 LILLPNGIDNRGSAPSPSITLLKLLSEFKLCQOE  
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 NGSATLFPPEHPMYKALKLEVSNI  
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 FGEKINFTHFYENRNDYHIEHYGYRFEQKPMYS  
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gene 189397..192990

CDS 189397..192990

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 proteins"  
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 FEQSINNSRLTEKSVKSALQSYLI  
 SYEKLAIQIDTIKELYVENIKTHFFLGKTRSPCQ  
 YYWRSGEQLSNDSSHLLRWSEWKKV  
 NCNINGTEEKFFINLSWHRSSLYIDWINKFSIRT  
 DKDETTEKYHYNRVYKNDNDTWSE  
 LIINMDIGFKLSTSTEVITLPPFFVNQGDPAKE  
 EVENLFLTNGTSIKRIESRLHGYI  
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 KISLLSPNSLPLKEKFQTSVDELL



gene 192987..197537  
CDS 192987..197537

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extracellular functions; secreted  
proteins"  
/note="residues 21 to 1511 of 1516  
are 48.90 pct identical to  
residues 1 to 1473 of 1476 from  
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 DNYLCLPLALRRWRQNNLLITGVGLTLKNPMR  
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 TLAESDGFGRVLLSARRVETGPSYSFDPENGLLV  
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gene 197671..197973  
 CDS 197671..197973

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gene 197977..198387  
 CDS 197977..198387

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CDS	198375..198743	
gene	198730..198903	
CDS	198730..198903	
gene	198944..201775	
CDS	198944..201775	

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GenPept : >gb|AAL18492.1|
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luminescens]"
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gene 201800..204658

CDS 201800..204658

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extracellular functions; secreted
proteins"
/note="residues 13 to 723 of 952
are 52.56 pct identical to
residues 12 to 716 of 760 from
GenPept : >gb|AAL18492.1|
(AF346500) unknown [Phototrhhabdus
luminescens]"
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/product="putative toxin subunit"
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gene 204594..204800  
 CDS 204594..204800

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 /note="residues 1 to 65 of 68 are  
 27.69 pct identical to residues  
 146 to 210 of 237 from GenPept :  
 >emb|CAB73875.1| (AL139078)  
 putative integral membrane protein  
 [Campylobacter jejuni]"  
 /codon-start=1  
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 /db-xref="GI:21956864"  
 /translation="MLFPYIDILIFYIQENILHH  
 YNLLILNTFPILNREGVYTRNTDF  
 LKSLILTAALAKIGLTNIPMLCWH"  
 /gene="t1dD"

gene complement(204861..2063  
 06)

CDS complement(204861..2063  
 06)

/locus-tag="y0193"  
 /gene="t1dD"  
 /locus-tag="y0193"  
 /function="phenotype; Not  
 classified"  
 /note="suppresses inhibitory  
 activity of CsrA; residues 1 to  
 481 of 481 are 84.40 pct identical  
 to residues 1 to 481 of 481 from  
 E. coli K12 : B3244; residues 1 to  
 481 of 481 are 84.61 pct identical  
 to residues 1 to 481 of 481 from

GenPept : >gb|AAL22237.1|  
 (AE008855) suppresses inhibitory  
 activity of CsrA [Salmonella  
 typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
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 protein"  
 /protein-id="AAM83787.1"  
 /db-xref="GI:21956865"  
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 LFSVLGQLTERRLDYADLYFQSSY  
 HEAMVLEDSIIKDGSYNDIQGVGVRAVSSEKGTG  
 AYADQITLNLQQAHAARSIVRD  
 TGNGKVHTLGEIAYQALYPLLDPLQSLRSREDKIA  
 LLHRVDKVARAADKRVQEVASLT  
 GVYEQILVAATDGTILAADVRPLVRLSVSVLVEDN  
 GKREGRACGGGGRFYDYFLETVD  
 GEVRADNFANEAVRMLVNLSAIAAPAGAMPVVL  
 GAGWPGVLLHEAVGHLEGDFNRR  
 GSSVFSGQMGKLVASELCTVDDGTMQGRGSLA  
 IDDEGVPGQYNNVLIEGILKGYMQ  
 DKLNARLMGVAPTGNRRRESYAHLPMPRMTNTYM  
 LAGQSTPEDIASVEYGLYAPNFG  
 GGQVDITSGKFVFTSEAYLIEKGKITHAVKGAT  
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 VGVCGKEGQSLPVGVGQPTLKLNLTVGGTA"  
 /locus-tag="y0194"

gene complement(206318..2071  
87)

CDS complement(206318..2071 /locus-tag="y0194"  
87)

/function="enzyme"  
 /note="residues 6 to 270 of 289  
 are 48.49 pct identical to  
 residues 4 to 266 of 275 from  
 GenPept : >gb|AAF93594.1|  
 (AE004129) conserved hypothetical  
 protein [Vibrio cholerae]"  
 /codon-start=1  
 /transl-table=11  
 /product="putative carbon-nitrogen  
 hydrolase"  
 /protein-id="AAM83788.1"  
 /db-xref="GI:21956866"  
 /translation="MKNANVALLQLCSGENTRDN  
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 WIQVGSMPMVSRSPDLITSSLL  
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 QPGQQLTVVDTPVGRGLMTICYDL  
 RFPGLFQALRAQAEIISVPAFTKMTGEAHWET  
 LLRARIENQCVCILAAQVGRHGA  
 TRRTWGHTMAVDWAGKIIHGNPDVAVALKVRIET  
 AGLKTI RNQMPVMQHNRFQATLEP  
 TLNKP LLNKPSPN"  
 /locus-tag="y0195"

gene complement(207184..2103  
75)

CDS complement(207184..2103 /locus-tag="y0195"  
75)

/note="residues 37 to 1062 of 1063  
 are 48.00 pct identical to  
 residues 1 to 985 of 986 from E.

coli K12 : B3245; residues 1 to 1056 of 1063 are 49.00 pct identical to residues 244 to 1259 of 1266 from GenPept :  
 >gb|AAL22238.1| (AE008855) paral putative protease [Salmonella typhimurium LT2]"  
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 /db-xref="GI:21956867"  
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 RIGPLLPTLSPTPELLARWADLPQGYVDALAL  
 DIPISQFETTRFQAKWHDVSWQYW  
 GQLPGVNHFDGELSGSARLGRNLNKNLLPYG  
 DLFAPLEVSQASGALNWRIDDKG  
 WALWSDQLDVQAKSLWGNQSFYMQPNQKPSQLN  
 QAQFWLKILAGIRLYDATDAWRYF  
 PVSMLGKELADYLTEALQGGQVDNATLVYNGNPH  
 DFPYKNKEGQFQVYVPLRNAVFQF  
 QPDWPDALDNLAIDLNFLNEGLWMNAPHLLGKVI  
 GSNISAIIPDYLKEKLYVDADVLG  
 EGRDVHDYFATPLKDSVAETLDELQVGGKISGR  
 LHLDIPLEESITHASGEVTLNNN  
 SLLVKPLQSQLENINGKFRFYDGNLESETLSANW  
 YGQPLTVNFTTKEQPKDFLVNVGL  
 QGDWLPKALPGVPDSLAKMLSGSANWQGVAVKL  
 PQHGKPDYQVDVSADLKKVSHLP  
 SPLDKNSGOALPLHVQVNGLEAFTLSGSAGNNN  
 AFNSQWLLQGEKVELARAINQTDTS  
 KKIPSLPDDKALVFKLPAIDGERWLALLAPELAT  
 AASPFAASFSSPSATSTQPKIKG  
 SKTNVILPKRLTLQTPPELLVGGQAWHQLTLQADP  
 LPSGMKITAKGQEVDSGLMADYG  
 PWHADLNLYYNPQWGSREANNPLAQAVSQEPTV  
 LQKPQPPSGISFSDWPALQLRCKA  
 CWILGQNIGRVNADLTPKGSALILNGLIEAGNG  
 RANITGOWQDQDRAGDKTTLNIGLN  
 GPRIDETLSFFGLTTLIKNASFAINADLNWRGVP  
 WEPQINTLSGTLKGRLGKGLTDL  
 GGGRAGQLRLVSDALLRLQLDFSDTFSRDFFA  
 FDSIRSTATLKNQVMSTNDLVIDG  
 LAADIAMNGKVDLVRQIAMEAVITPELSATVGV  
 ATAFAINPIVGAAVFAASKILGPL  
 WSKVSLIRYQITGSLDQPTIHEVLRLQKENEAP"

gene complement(211201..212670)

CDS complement(211201..212670)

/gene="cafA"  
 /locus-tag="y0196"  
 /function="structural component;  
 cell division"  
 /note="residues 1 to 489 of 489 are 90.18 pct identical to residues 7 to 495 of 495 from E. coli K12 : B3247"  
 /codon-start=1

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/transl-table=11
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protein"
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/db-xref="GI:21956869"
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CVAGDEQKNFNVVDIAELVRQGD
LMVQVVKDPLGTGKARLTITLPSRYLVLMPGA
AHVGVSQRIESEAEERERLKKTVAA
YCDEQGGFIIRTAEGIGEEELSADAFLKRLWT
KVQERKKRNITKYKLYGEMALAQR
VLRDFAGAALDKIRVDSKLTYYDLLVEFTREIPE
MTDKLELYTGKQPIFDLYDVENEI
QRSLEKVELKSGGYLIIDQTEAMTTVDINTGAF
VGHRNLEETIFNTNIEATQAIARQ
LRMRNLGGIIIIIDFIDMSNEDHRRRVLHSLEQAL
SKDRVKTSLNGFSQLGLVEMTRKR
TRESIEHVLCEHCPCTCRGRGTVKSVEVTCYEILR
EIVRVHHAYDSRFLVYASPAVGE
ALKGEESHALAEVEIFVVGKQVKQIEPLYNQEQF
DVVMM"
gene      complement(212660..2132 /locus-tag="y0197"
59)
CDS       complement(212660..2132 /locus-tag="y0197"
59)

/notes="residues 3 to 198 of 199
are 70.40 pct identical to
residues 1 to 196 of 197 from E.
coli K12 : B3248"
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/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83791.1"
/db-xref="GI:21956870"
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LLDLPFEVLKTEVEEQRHGPESAQ
VYVQRLAQDKARAGVAVAPQDLFVLGADTIVVLN
GQVLEKPRDKHAQQILSALSGQK
HQVMTAVALADRONMLSAMVVTDTVTFRVLSPLEI
SDYIATGPEMDKAGAYGIQKGGC
FVRAIAGSYHAVVGLPLVETHELLSHFIAQRNVR
GIHDS"
gene      212878..213480 /locus-tag="y0198"
CDS       212878..213480 /locus-tag="y0198"

/notes="residues 23 to 126 of 200
are 29.80 pct identical to
residues 226 to 324 of 454 from
GenPept :
>gb|AAF11838.1|AE002061-5
(AE002061) cell wall
glycyl-glycine endopeptidase,
putative [Deinococcus
radiodurans]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83792.1"
/db-xref="GI:21956871"
/translation="MSHLSQFPWITCFADRPTPR
RSPDASGQTMHSVFVVHVPVWV

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FLKPAHLTPQWYRHPIPVNPVVRQPHLPVLYPAP
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SGRNATLITKNSDQNTTTSIVSESSMTISACCHS
AILRNN"
gene      complement(213267..2137 /gene="mreD"
55)
CDS      complement(213267..2137 /gene="mreD"
55)
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        /function="structural component;
        murein sacculus, peptidoglycan"
        /note="residues 1 to 162 of 162
        are 75.30 pct identical to
        residues 1 to 162 of 162 from E.
        coli K12 : B3249; residues 4 to
        162 of 162 are 77.35 pct identical
        to residues 5 to 163 of 163 from
        GenPept : >gb|AAL22241.1|
        (AE008855) rod shape-determining
        protein [Salmonella typhimurium
        LT2]"
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        /transl-table=11
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        /db-xref="GI:21956872"
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        QALIVMLSLTMDVVVWFSEFLVINVAFRPEVFW
        SSVVNGILWPWFLFLMRKIRRFQFS VQ"
gene      213735..213854
CDS      213735..213854
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        /note="residues 2 to 38 of 39 are
        44.73 pct identical to residues 73
        to 110 of 118 from GenPept :
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        unknown protein [Mesorhizobium
        loti]"
        /codon-start=1
        /transl-table=11
        /product="hypothetical"
        /protein-id="AAM83794.1"
        /db-xref="GI:21956873"
        /translation="MTTVTIHGETPGVTTPGVAP
        AGVDAAGAGGPIASAEQNT"
gene      complement(213752..2147 /gene="mreC"
47)
CDS      complement(213752..2147 /gene="mreC"
47)
        /locus-tag="y0201"
        /locus-tag="y0201"
        /function="structural component;
        murein sacculus, peptidoglycan"
        /note="residues 1 to 316 of 331
        are 81.32 pct identical to
        residues 1 to 316 of 367 from E.

```

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coli K12 : B3250; residues 1 to
327 of 331 are 80.30 pct identical
to residues 1 to 330 of 350 from
GenPept : >emb|CAD07888.1|
(AL627278) rod shape-determining
protein [Salmonella enterica
subsp. enterica serovar Typhij]
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protein"
/protein-id="AAM83795.1"
/db-xref="GI:21956874"
/translation="MKPIFSRGPSLQLRLFFAI
AAIVLVIADSRIGTFVKIRTYMDT
AVSPFYFLANGPRKILDNVSDTLATREQLELENR
ALRQELLLKNTDLQLLGQFKQENN
RLRELLGSPLRQDEQKMTQVMSSGTDPSYDHVV
IDKGSNSGVYEGQPVISDRGVVGQ
VVAVSKFTSRVLLICDASHALPIQVLRNDIRVIA
AGSGCSDDLLLEHLPSTNDRVIGD
VLVTSGLGGRFFEGYPVAVVSVKVDNQRAYTVI
QARPTADLQRLRYLLLLWGADRNG
DMPMPPEVRRVANERLAPMMSQVLPSADAMGPP
APAASTPAGATPGVVTGPVSP"
gene      complement(214951..2159 /gene="mreB"
94)

CDS      complement(214951..2159 /locus-tag="y0202"
94)      /gene="mreB"

/locus-tag="y0202"
/function="phenotype; cell
division"
/notes="septation function;
residues 1 to 347 of 347 are 99.13
pct identical to residues 21 to
367 of 367 from E. coli K12 :
B3251; residues 1 to 347 of 347
are 100.00 pct identical to
residues 1 to 347 of 347 from
GenPept : >emb|CAC93135.1|
(AJ414158) rod shape-determining
protein MreB [Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="regulator of ftsI,
penicillin binding protein 3"
/protein-id="AAM83796.1"
/db-xref="GI:21956875"
/translation="MFKKFRGMFSNDLSIDLGTA
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EMRPSPRVLVCVPVAGATQVERRAIRESAQGAGAR
EVFLIEEPMAAAIGAGLPVSEATG
SMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRF
DEAIINYVRRNYGSLIGEATAERI
KHSIGSAYPGDEVLEIEVGRNLAEGVPRGFTLN
SNEILEALQEP LTGIVSAVMVALE
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TGIPVVVAEDPLTVCVARGGGKALE
MIDMHGGDLFSEE"

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gene      complement(216331..2182 /locus-tag="y0203"
47)
CDS       complement(216331..2182 /locus-tag="y0203"
47)

/notes="residues 1 to 638 of 638
are 50.70 pct identical to
residues 1 to 641 of 646 from E.
coli K12 : B3252; residues 1 to
638 of 638 are 50.70 pct identical
to residues 1 to 641 of 646 from
GenPept :
>gb|AAG58379.1|AE005553-1
(AE005553) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
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/protein-id="AAM83797.1"
/db-xref="GI:21956876"
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IVTAYDQSLLLQPINKKREWLPMMQTLGVVDVS
VKNSTSTLYQLHPIAVYTPWNSHS
RYRQMVLP LLHOPGTEMHFNYIDPLGSYARSIIYA
AAILSLVVVVIALLTLLSFRWLRD
QTVGQEKLERRARRILNGEREHAVRSEDYEWPPC
ASRAIDHLLSELMEVRAERNRVD
LIRTFAAQDAQTGLSNRQFFDNQLTQLEETGAH
GVVMVQLPDFEALNETHDQQQVQ
ELMSSLVNLLSTFVARYPSALLARYLNSDIAILL
PHKTLKDADVMAAQLVNAVRTLPE
PHIIDRESLLHIGIVAYRSGESVEQIMDNAGQAT
KSAALYGGNGWYVDTQVPERGRG
SVKWRITLLEQTLASGGPRLYQKPVITVDGKISHR
EIISRIYDGEQELAAEFMPLVQL
LGLGERYDRQKIDKIIPLLSLWPDETLAFSISVD
SLLHRFPQRWLRD LLOCKKSDRM
RIIFELAEADVCOHIEIRQMVRLLRGVGVCKVMA
SQAGLTVVSTSYIKSLQVEMIKLH
PGVVRISINFRYENQLFVESLTGACAGTQTKVFAA
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/locus-tag="y0204"
/locus-tag="y0204"
/notes="residues 1 to 324 of 325
are 74.38 pct identical to
residues 1 to 323 of 324 from E.
coli K12 : B3253; residues 1 to
324 of 325 are 74.69 pct identical
to residues 1 to 323 of 324 from
GenPept :
>gb|AAG58380.1|AE005553-2
(AE005553) putative dehydrogenase
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative dehydrogenase"
/protein-id="AAM83798.1"
/db-xref="GI:21956877"
/translation="MRALILEQIEGRRTTAEVRQI
SASQLPAGNVTVDVNWSSSLNYKDA

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gene 219764..220948  
CDS 219764..220948

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STATAILLSALGYIAAISGRDSNSDYLNKLGQAQR  
ILPRSDYLDASRPLEKQLWAGAI  
TVGDSMLAKILAQMNYNGTVAACGLAGGYNLPTT  
VMPFILRNIRLQGVDSVMTPOPRR  
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/locus-tag="y0205"  
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/note="residues 62 to 394 of 394  
are 75.44 pct identical to  
residues 1 to 334 of 334 from E.  
coli K12 : B1971; residues 62 to  
394 of 394 are 79.04 pct identical  
to residues 1 to 334 of 334 from  
GenPept : >gb|AAL22246.1|  
(AE008855) putative nitrate  
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LT2]"  
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/db-xref="GI:21956878"  
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SI  
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ALTPEDKVTGYNNFYFGLDKADP  
AANAGTLKTEDWQIKIDGDVVKPMTLMDYLMKC  
FPLEERIYRLRCVEAWSMVVPWIG  
FELGKLLKLAEPSTNARYVAFQTLYAPDQMPGQK  
NRFIGGGLDYPYVEGLRLDEAMHP  
LAFMVVG VYGKTLFPQNGAPLRLMTFWKYGFKSI  
KSI  
IVHIRLIRDPPTTWNLSAPNE  
YGFYANVNPVHDHPRWSQATERVIGSGGILDVKR  
OPTLLFNGYAEQVASLYRGLDLRK NF"  
/locus-tag="y0206"  
/locus-tag="y0206"  
/note="residues 1 to 203 of 206  
are 68.96 pct identical to  
residues 1 to 203 of 211 from E.  
coli K12 : B1972; residues 1 to  
206 of 206 are 72.81 pct identical  
to residues 1 to 199 of 199 from  
GenPept : >emb|CAD07893.1|  
(AL627278) putative membrane  
protein [Salmonella enterica  
subsp. enterica serovar Typhi]"  
/codon-start=1  
/transl-table=11  
/product="hypothetical protein"  
/protein-id="AAM83800.1"  
/db-xref="GI:21956879"  
/translation="MRLSLRHITWLKIAIWLAA  
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LLGLWCFAWGTLHLLSYSILELGL

gene 220948..221568  
CDS 220948..221568

gene	221831..222283	SNIGLLGHELINRPYLTLGIISWLVLALALALTST RWAQRKMGARWQKLHNWVYVAIL APIHYLWSVKTLSPWPIIYAVMAALLLLRYKLL LPRYKKFRQWFR"
CDS	221831..222283	/locus-tag="y0207" /locus-tag="y0207" /function="enzyme" /note="residues 1 to 146 of 150 are 73.28 pct identical to residues 1 to 146 of 149 from GenPept : >gb AAD10235.1  (AF011408) type II 3-dehydroquinase [Aeromonas salmonicida subsp. salmonicida]" /codon-start=1 /transl-table=11 /product="putative dehydroquinase" /protein-id="AAM83801.1" /db-xref="GI:21956881" /translation="MSDKFHILLNGPNLNLGTT REPEKYGYTTLAEIVSQLEIQAGG MDVALSHLQSNAAHALIDSIHQARGNTDFILINP AAFTHTSVALRDALLGVQIPFIEI HLSNVHAREPFRHHSYLSDIAVGVICGLGADGYN FALQAAVNRLSKSN" /gene="accB" /locus-tag="y0208" /gene="accB" /locus-tag="y0208" /function="carrier; biosynthesis of cofactors, carriers: biotin carboxyl carrier protein (BCCP)" /note="carrier of biotin; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from E. coli K12 : B3255; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from GenPept : >gb AAL22248.1  (AE008856) acetylCoA carboxylase, BCCP subunit, carrier of biotin [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="acetyl CoA carboxylase, BCCP subunit" /protein-id="AAM83802.1" /db-xref="GI:21956882" /translation="MMGIIATHKEYGITLMDIRK IKKLIELVEESGISELEISEGEES VRISRAFAAPNYPMMQOPYAFAPQQPALAAAV APAPVAEAPAAISGHIVCSPMVG TFYHTPSPDAKAFVEVGQKVSVDGLTCIVEAMKM MNQIEADKSGTVKAILVENGQPVPE FDEPLVVIE" /gene="accC" /locus-tag="y0209" /gene="accC" /locus-tag="y0209" /function="enzyme; fatty acid and phosphatidic acid biosynthesis"
gene	222396..222905	
CDS	222396..222905	
gene	222917..224266	
CDS	222917..224266	

gene	225624..225866	/note="residues 1 to 448 of 449 are 92.41 pct identical to residues 1 to 448 of 449 from E. coli K12 : B3256" /codon-start=1 /transl-table=11 /product="acetyl CoA carboxylase, biotin carboxylase subunit" /protein-id="AAM83803.1" /db-xref="GI:21956883" /translation="MLDKIVIANRGEIALRILRA CKELGIKTVAVHSVADRLDKHVL ADETVCIGPAPSVKSYLNIPAIISAAEITGAVAV HPGYGFLSENADFAEQVERSGFIF IGPRAETIRLMGDKVSAISAMKKAGVPCVPGSDG PLSDDTTKNKFAKRIQYGPVIIKA SGGGGGRGMRVVRHDKDLEESINMTRAEAKA NDVMYMEKYLENPRHIEVQILADG QGNAIYLAERDCSMQRRHQKVVEEAPAPGITSEM RRYIGERCAKACMEIGYRGAGTFE FLYENGEFYFIEMNTRIQVHTVTMITGIDLK EQLRIAAGQPLSIKQDEVKVHGA VECRINAEDPNTFLPSGKITRFHAPGGGVRWE SHIYAGYTPPPYYDSMIGKLITYG ENRDAIARMKNALAEIIDGKTNVELQQRIMN DENFQHGGINIHYLEKKLGLQET" /locus-tag="y0210" /locus-tag="y0210" /note="residues 1 to 79 of 80 are 68.35 pct identical to residues 1 to 79 of 80 from E. coli K12 : B3257; residues 1 to 79 of 80 are 69.62 pct identical to residues 1 to 79 of 80 from GenPept : >gb AAG58385.1 AE005553-7 (AE005553) orf, hypothetical protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83804.1" /db-xref="GI:21956884" /translation="METRFLQANKEARWAFGLTL AYLAGWIITAYLPGNLPGMSGFLPA WFEEACIALPLLFIVLCILMVRILFRDIPLED DDAN" /gene="panF" /locus-tag="y0211" /gene="panF" /locus-tag="y0211" /function="transport; transport of small molecules; cations" /note="residues 1 to 472 of 486 are 82.83 pct identical to residues 1 to 472 of 485 from E. coli K12 : B3258" /codon-start=1 /transl-table=11 /product="sodium/pantothenate symporter" /protein-id="AAM83805.1"
CDS	225624..225866	
gene	225850..227310	
CDS	225850..227310	

		<pre> /db-xref="GI:21956885" /translation="MTMQTDVVLPLVGYLVLVFG LSIYAYTRRQTGNFLNEYFIGNRS MGGFVLAMTLTATYISASSFIGGPGAAYKYGLGW VLLAMIQLPAVWLSLGLVGKFAI LARRYNAVTLNDMLYARYQSRLLVWLASISLLVA FVGAMTVQFIGGARLLETAAGIPY DTGLLIFGISIALYTSFGGFRASVLNDALQGLVM LIGTILLLVAVIHAAGGLHKAVET LQHIDPALVSPQGGDQILDVPPMASFWILVCFGV IGLPHATAVRCISYRDSKAVHRGII LGTIVVAILMFGMHLGALGRAVLPLDKIPDQVI PTLMITVLPPFAAGIFLAAPMAAI MSTINAQLLQSSATIVKDLYNLWPAELKNERKL ARISSLSTLILGLLLLLAAWRPPE MIIWNLNLAFFGGLLEAVFLWPLVLGLYWERANAHG ALSAMIVGAVCYTVLASFDIKIAG LHPVPSLTNLNLAFFYIGNLFGDRARARHPAIVS AD" </pre>
gene	227347..228267	/gene="prmA"
CDS	227347..228267	<pre> /locus-tag="y0212" /gene="prmA" /locus-tag="y0212" /function="enzyme; ribosomal proteins - synthesis, modification" /note="residues 14 to 305 of 306 are 85.27 pct identical to residues 1 to 292 of 293 from E. coli K12 : B3259" /codon-start=1 /transl-table=11 /product="methylase for 50S ribosomal subunit protein L11" /protein-id="AAM83806.1" /db-xref="GI:21956886" /translation="MVMAPIPALERIAMPWIQLK LNTIGNQAESLGDVLVESGAVSVT FQDTHDNPVFEPLPGETRLWGDIDVIGLYDAETD MADVAMLECHPQIGKGF IHKIEQ LEDKDWEREWMDNFHMPRFGERLWICPSWRDVPD PTAVNVMLDPGLAFGTGHTPTAL CLQWLDSLDLNGKTLIDFGCGSGILAIAALKLGA ARAIGIDIDPQAIQASRDNAQRNG VSRLELYLAKDQPAELSDVTVVANILAGPLREL APLISVLPTTGGHGLSLGVLATQA AGVAQAYEDKFI LDPVAEKEEWCRITGIKK" </pre>
gene	228754..229821	/locus-tag="y0213"
CDS	228754..229821	<pre> /locus-tag="y0213" /note="residues 35 to 355 of 355 are 87.85 pct identical to residues 1 to 321 of 321 from E. coli K12 : B3260; residues 35 to 355 of 355 are 92.21 pct identical to residues 1 to 321 of 334 from GenPept : &gt;gb AAC77880.1  (AF040378) yhdG homolog [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="putative dehydrogenase" /protein-id="AAM83807.1" </pre>

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/db-xref="GI:21956887"
/translation="MLFFHQLVKVPFIWAQKCV
IYAPLRTQCGHSLSMRIGHFQLTN
CLIAAPMAGITDRPFALCHGMGAMVSEMLSS
NPEVVRTDKSRLRMVHVDEPGIRN
VQIAGNDPDEMAAAARINVASGAQIIDINMGCPA
KKVNRKLAGSALLQHPDLVKQILS
AVVNAVDPVPTLKIRTGWSPEHRNCIEIAQLAEN
CGIQALTIHGRTRSCLFNGEAEYD
SIRAVKQTVSIPVIANGDITDPHKARAVLDYGA
DALMIGRAAQGRPWIFREIQHYLD
TGELLPPMPLGEVQRLLDGHIRELHDFYGPQKGF
RIARKHVSWYLQEHAPNDQFRRTF
NAIEDASEQLEALEAYFENLA"
gene      229846..230142 /gene="fis"
CDS       229846..230142 /locus-tag="y0214"
          /gene="fis"
          /locus-tag="y0214"
          /function="factor; DNA -
          replication, repair,
          restriction/modification"
          /note="DNA-binding protein; a
          trans activator for transcription;
          residues 1 to 98 of 98 are 97.95
          pct identical to residues 1 to 98
          of 98 from E. coli K12 : B3261"
          /codon-start=1
          /transl-table=11
          /product="site-specific DNA
          inversion stimulation factor"
          /protein-id="AAM83808.1"
          /db-xref="GI:21956888"
          /translation="MFEQRVNSDVLTVATVNSQD
          QVTQKPLRDSVKQALKNYFAQLNG
          QDVSDLYELVLAEEVQPLLDMVMQYTRGNQTRAA
          LMMGINRGTLRKLLKKYGMN"
gene      complement(230896..2313
72)
CDS       complement(230896..2313 /locus-tag="y0215"
72)
          /locus-tag="y0215"
          /note="residues 13 to 88 of 158
          are 33.70 pct identical to
          residues 4 to 89 of 134 from
          GenPept : >dbj|BAB04617.1|
          (AF001510) BH0898 unknown
          conserved protein in B. subtilis
          [Bacillus halodurans]"
          /codon-start=1
          /transl-table=11
          /product="hypothetical"
          /protein-id="AAM83809.1"
          /db-xref="GI:21956889"
          /translation="MNTENKKLSTLIGKIHTIAK
          SRLAAGYEDRNGINEHQVTPCHHA
          LTLGGDDFAESYLPFLRNNGFDLNGVRLFGFY
          DDKGDERDLRKQLADLKAPPELFP
          DAFNDWVLIGETDIDILFNKNGSYENRDRIGL
          DRLNESYDDIVGLLISLPLIE"
gene      complement(231438..2321
63)
CDS       complement(231438..2321 /locus-tag="y0216"
63)
          /locus-tag="y0216"

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/function="regulator"
/note="residues 29 to 231 of 241
are 36.71 pct identical to
residues 9 to 215 of 223 from
GenPept : >dbj|BAB53015.1|
(AP003010) transcriptional
regulator [Mesorhizobium loti]"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="AAM83810.1"
/db-xref="GI:21956890"
/translation="MFCITEAWYKKQPYCRTGIQ
LMLAGMGVIKPETLRYQVENVLRLQ
AIMSGRFTPGERLIERELCETLGVSRTSIREALR
RLEAEKLVSIIPHKGPIVAIISRO
EAAELFALRGLLEGFAAREFAQRATDVAIVHFAQ
AIQALRMAGMTKDRAKVLKAKTDL
YDVLLDNCGNGLVKETLTSLHSRINLLRATSLMD
PQRLPVSINEIDDLYQALKARDFD
AAERHVANAKEVALRILEETNAT"
gene      complement(232190..2335 /locus-tag="y0217"
54)
CDS       complement(232190..2335 /locus-tag="y0217"
54)

/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 31 to 444 of 454
are 26.35 pct identical to
residues 35 to 452 of 461 from
GenPept : >dbj|BAB60327.1|
(AP000995) shikimate transporter
[Thermoplasma volcanium]"
/codon-start=1
/transl-table=11
/product="putative metabolite
transport protein, permease"
/protein-id="AAM83811.1"
/db-xref="GI:21956891"
/translation="METLSADSAITAAENDPLRD
VKRKNAIKGAFFSEFIDMFDIYLP
VIVLPFVLFYFQFPNLSSTANILASLVFITLL
GRPIGALLFGIMADRIGRRMASIY
SVSGFGVVFTLIALIPGYETLGIASYLLLVLLRF
IDGIFLGGGYTGAIPALAEYSKKE
QRGFVGGILISGFPAAYVAINLVAMLMFALIPLD
GLYSPYAQWGWRIPFVIGGLLAGF
LALYYVFNVTESVWQOGSSKKRAREKQPLSTLV
SGQSGRNLMQVLLMMSGFWLTQNL
ITLFLPTGLLINTLNMRLQVTSILLVTYCVLFF
SYIGMGMLGQKIGRRRFFMIAGPL
IATMGSAALLYVLSHGDGLSFSTVMLLVCLLAVVV
TSPGVIIITYINEHFATGVRATGF
GVGFSLSVIIIPSFYAFYMDWLSVVVPFELTAVVL
LALGGMIGTVGAIMGPETKEVDFT SSAG"
gene      complement(233708..2341 /locus-tag="y0218"
45)
CDS       complement(233708..2341 /locus-tag="y0218"
45)

/function="enzyme"

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/feature="residues 21 to 141 of 145
are 48.36 pct identical to
residues 15 to 136 of 139 from
GenPept : >gb|AAK42990.1|
(AE006881) 4-carboxymucolactone
decarboxylase (pcaC) [Sulfolobus
solfataricus]"
/codon-start=1
/transl-table=11
/product="putative decarboxylase"
/protein-id="AAM83812.1"
/db-xref="GI:21956893"
/translation="MSNRVGYEIGRRVMMVAQDR
FERGFHNRKVVVLGAEHVETSWGNS
DEFNRPVQKLITEYCWGEVWGDPALTFKTRSMNLN
IGILTAMGQHHELSLHVKGALRNG
VTREEIRAVLLQTVVYCGAPVALAAAFRIASAAIK
AYDDEIADS"
/locus-tag="y0219"

gene      complement(234281..2351
71)
CDS       complement(234281..2351 /locus-tag="y0219"
71)

/function="enzyme"
/feature="residues 6 to 290 of 296
are 34.58 pct identical to
residues 2 to 290 of 298 from
GenPept : >emb|CAD17800.1|
(AL646080) probable
3-hydroxyisobutyrate dehydrogenase
oxidoreductase protein [Ralstonia
solanacearum]"
/codon-start=1
/transl-table=11
/product="putative oxidoreductase"
/protein-id="AAM83813.1"
/db-xref="GI:21956894"
/translation="MKQLQRIGFIGLGKMGTPMV
QRLVKAGFELYLCDADITKQVILT
AELNAESLTVDNAASLDALITMLPNSEAVEQVLL
GSDGISGWVAQLSQAADVIMSSS
DPERSRRLAILLAVWELDYLDAPVSGGVKKAQNG
TSLILIGGEDRVLKSCTYALAMG
EQILFVGPAAGSGHAAKALNNYVSATGLLATIEAL
HVAQRFGIEPEVMTEVLNTSTGRS
NTSENKVRQFMLNGSYASGFTLQLMKNKDLHIARN
LAQRLNYPMRLGMHCVDVWDEVSR
RATPMADHTEMYRLLLIDKEP"
/locus-tag="y0220"

gene      complement(235236..2360
63)
CDS       complement(235236..2360 /locus-tag="y0220"
63)

/feature="residues 46 to 246 of 275
are 28.20 pct identical to
residues 34 to 254 of 262 from
GenPept : >gb|AAB89741.1|
(AE000998) A. fulgidus predicted
coding region AF1509
[Archaeoglobus fulgidus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83814.1"

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		<pre> /db-xref="GI:21956895" /translation="MENRDMASASHENYRIFAICY AHHHRLTRDNFLGGDPHDGMPID YFVVAIVGTRTTRIMVDTGFDAAMAHQGRITITHC IEDGLSQLGIDAGKIEDVIIISHMH YDHAGNHGLFPNARFHLQDREMAFCTGRCMGHGG LSQAFDVEDVKAMVGRFLFAGRLQF HHGDAEIAIPGISVHRVGGHTDGLQIIRVHTARGW VVLASDATHFYANIQQRRPYPILY NVGDVLEGYNTLYRWADSFHIIIPGHDPMLVQRY PAGITPETAAWIAQVDVAFLTQWT" /gene="slyB" /locus-tag="y0221" /gene="slyB" /locus-tag="y0221" /function="putative membrane" /notes="residues 3 to 157 of 157 are 66.02 pct identical to residues 1 to 155 of 155 from E. coli K12 : B1641; residues 3 to 157 of 157 are 73.71 pct identical to residues 1 to 155 of 155 from GenPept : &gt;emb CAA42977.1  (X60448) outer membrane lipoprotein [Yersinia enterocolitica]" /codon-start=1 /transl-table=11 /product="putative outer membrane receptor" /protein-id="AAM83815.1" /db-xref="GI:21956896" /translation="MIMNKLAIAVALAATVLSGC ANNTASGDTFTASQARQVQTVTYG SIVSARPVIIQGGNNNNVAGAIGGAVVGGFLGNT IGGGGNSLATAGGAVAGGVAGQG IQSAMNRSEGVQLEIRRDDGSNIVVQAQGPTRF SAGQRVIIASDRSGTVTVSPR" /locus-tag="y0222" </pre>
gene	236518..236991	
CDS	236518..236991	
		<pre> /notes="residues 41 to 57 of 65 are 76.47 pct identical to residues 1185 to 1201 of 1247 from GenPept : &gt;gb AAL20679.1  (AE008778) nitrate reductase 1, alpha subunit [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83816.1" /db-xref="GI:21956897" /translation="MVFSDFMGYVLHLMWINNL LRQLNACGNLCNIFGGGRAYHHFV THISPKPTHMIGGLRAISLRL" /gene="cspI" /locus-tag="y0223" /gene="cspI" /locus-tag="y0223" /function="phenotype; Not classified" </pre>
gene	237428..237736	
CDS	237428..237736	

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/note="residues 33 to 102 of 102
are 82.85 pct identical to
residues 1 to 70 of 70 from E.
coli K12 : B1552; residues 33 to
102 of 102 are 98.57 pct identical
to residues 1 to 70 of 70 from
GenPept : >emb|CAB10779.1|
(Z97978) hypothetical protein
[Yersinia pestis]"
/codon-start=1
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/protein-id="AAM83817.1"
/db-xref="GI:21956898"
/translation="MSLLLSAQVRHPLKDRPSRL
HYCGKIIEGNISMSNKMTGLVKWF
DAGKGFIFITADGSKDVFVHFSAIQSNDFKTL
EGQNVEFSIENGAKGPSAVNVIAL "
gene 237921..238208
CDS 237921..238208
/locus-tag="y0224"
/feature="cspI"
/feature="cspI"
/feature="cspI"
/function="phenotype; Not
classified"
/note="residues 26 to 95 of 95 are
84.28 pct identical to residues 1
to 70 of 70 from E. coli K12 :
B1552; residues 26 to 95 of 95 are
100.00 pct identical to residues 1
to 70 of 70 from GenPept :
>emb|CAB10779.1| (Z97978)
hypothetical protein [Yersinia
pestis]"
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/transl-table=11
/product="cold shock-like protein"
/protein-id="AAM83818.1"
/db-xref="GI:21956899"
/translation="MPHKFYPSLSSRLWRQLKII
EGSISMSNKMTGLVKWFDAGKGF
FITADGSKDVFVHFSAIQSNDFKTLDEGQNVEF
SIENGAKGPAAVNVIAL"
repeat-region complement(238285..2389
94) /note="insertion element"
/insertion-seq="IS1541a"
gene complement(238391..2389
00) /locus-tag="y0225"
CDS complement(238391..2389
00) /locus-tag="y0225"
/function="IS and transposon
related functions"
/note="IS1541a; residues 1 to 169
of 169 are 100.00 pct identical to
residues 1 to 169 of 169 from
GenPept : >gb|AAC82673.1|
(AF074611) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83819.1"
/db-xref="GI:21956900"

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gene	238849..239211	/translation="MRSGNCKCSTRNQKGVPMRD EKS LAHTRWNCKYHIVFAPKYRRQ VFYREKKRAIGSILRKLCEWKNVNILEAEYCVDH IHMLLEIPPKMSSVSGFMGLKGKS SLMLYEQFGDLKFKYRNREFWCRGYVDTVGKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK"
CDS	238849..239211	/locus-tag="y0226" /locus-tag="y0226" /note="residues 61 to 115 of 120 are 36.36 pct identical to residues 30 to 81 of 275 from GenPept : >gb AAL48672.1  (AY071050) RE13795p [Drosophila melanogaster]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83820.1" /db-xref="GI:21956901" /translation="MGPPFDLLNICSCQTANCF NKS KGVF ITDPK LKALLNPQPSWG FSGHKKNLPPCRFFCAYDTGTDIKNTALPRAPES PADIIAAQKNHVTGQETVIWNL TILAGSPFFIHLEQCETVV"
gene	239254..240429	/locus-tag="y0227"
CDS	239254..240429	/locus-tag="y0227" /note="residues 1 to 388 of 391 are 58.50 pct identical to residues 1 to 388 of 391 from GenPept : >gb AAL19518.1  (AE008722) putative ATPase involved in DNA repair [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83821.1" /db-xref="GI:21956902" /translation="MKKLIKRLEIISKGIELEDD DIIRHQLPYLKSETQDPVLVFIWM AIEQGKFTQALDAIATWLGSKQGVIQWQDIELAA CKLELKALEEQLSLIDKRNERTQ LLDDFNDLYLVRLGPLMKQILNLRQLAESTLRK AEAEARRRRERYRNCQQYISQAID ELISLKQRWLALPSISNDTIEIRNRIQQQTELIT ALLAEIKELENSFCTRNTSTRKA REEAKEKYERYQEQTDAEQRLDNRKLSSEQRQ DLKRLWRQASRLCHPDLVADAFKE KAHQLMVQLNQARQRGDFPAIHALLLES LKQGLEP LMAADLIDDLERLRKISDVRTQI DAIHLEIDALKGEESWRLATSLPDKDKWFKEQEN VLSKTLNILERQVEEASRVLYEA"
gene	complement(240536..2418 82)	/locus-tag="y0228"
CDS	complement(240536..2418 82)	/locus-tag="y0228"  /note="residues 3 to 446 of 448 are 52.78 pct identical to residues 1 to 449 of 452 from GenPept : >emb CAC45768.1  (AL591786) hypothetical signal

peptide protein [Sinorhizobium  
meliloti]"

/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83822.1"  
/db-xref="GI:21956903"  
/translation="MHMSKFRVLVLLASSIAFSTS  
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ATPSDAPTDLQQSGKYTSGQRVSALGSVAAKSAD  
RLTGIGLPISSGQPLQGHSGIKHMP  
DGTYWVLTDNGFGSKANSPDAMLYLNHYNIDFKN  
GNVITPLQTVFLHDPDKKVPFHHIN  
ESTEKRYLTGSDFDPESEFQFADDALWIGDEFGPY  
LIKADLNGKVLAVFETQVDGNVVK  
SPDNFTLTLPGAPDGKQNFQVARSKGFEGBAVSP  
DGSKLYPMLEGALWDGEKFENIDG  
KRYLRVLEFDVKNQAWTGRSQYVLEDNQNAIGD  
FNLIDANHGLVIERDNGEGTADKA  
CAAGAPTDKCFQIAKFKRVYKIAFSDDNVGKPV  
EKVSYIDLLNIKDPQNLARKPLNN  
GVLTFFPFTTIENVVDVDAHIIVGNDNNFFPSSS  
ROPNEADDNEFILLDVKALLSQ"

/locus-tag="y0229"  
/locus-tag="y0229"  
/note="residues 2 to 280 of 284  
are 70.25 pct identical to  
residues 17 to 295 of 304 from E.  
coli K12 : B2989; residues 2 to  
280 of 284 are 72.04 pct identical  
to residues 1 to 279 of 288 from  
GenPept : >gb|AAL22014.1|  
(AE008844) putative glutathione  
S-transferase [Salmonella  
typhimurium LT2]"

/codon-start=1  
/transl-table=11  
/product="hypothetical protein"  
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HLIRISEGEQFSSGFVSINPNSKI  
PALMDYSSTPPVRVFESGAILLYLADKFGHFLPK  
SHAARTEALNWLFWLQGAAPYLG  
GFGHFYHYAPVKIEYIDRFTEAKRQLDLLNTQ  
LKTHEYIAGDEYTIADIAIWPWYG  
SLVLGLQYEAGEFLDVKSYPHLIRWTETIAKRPA  
VQRGRIVNRTWGAPEEQLPERHDA ADFDRLIK"

/locus-tag="y0230"  
/locus-tag="y0230"  
/note="residues 14 to 194 of 201  
are 44.75 pct identical to  
residues 14 to 194 of 200 from  
GenPept : >emb|CAC95734.1|  
(AL596165) similar to putative  
sugar-phosphate isomerase  
[Listeria innocua]"

/codon-start=1

gene 242133..242987  
CDS 242133..242987

gene complement(243177..243782)  
CDS complement(243177..243782)

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NSDELTRLPLTLQRKQVKIISVTENEQSAIAQVS
ALVLKTHVKQEIPLNMLATTISV
LVLALFDAICACLMARTGFSKETLLAVHPGGDVG
MVLKQQ"
gene      complement(243779..2454 /locus-tag="y0231"
31)
CDS       complement(243779..2454 /locus-tag="y0231"
31)

/function="enzyme"
/note="residues 8 to 548 of 550
are 50.44 pct identical to
residues 13 to 566 of 569 from
GenPept : >emb|CAB81024.1|
(AL161576) putative protein
[Arabidopsis thaliana]"
/codon-start=1
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KGLGFDAATCSLVVLDKEGNPLTVS
PSGRNEQNQVIVWMDHRAITQAEINATKHPVLEF
VGGVISPQMOTPKLLWLKQHMPT
WSNVGHLFDLPDFLTWRATKDETRSLCSTVCKWT
YLGHEDRWDPSYFKLVGLADLLDN
NAAKIGATVKPMGAPLGHGLSQRAASEMGLIPGT
AVSVSIIDAHAGTIGILGASGVGT
ENANFDRRIALIGGTSTAHMAMSRSAHFISGIWG
PYYSAILPEYWLNEGGSATGALI
DHIIQSHPCYPALLEQAKNKGETIYEALNYILRQ
MAGEPENIAFLINDIHMPLPYFHGN
RSPRANPNLTGIITGLKLSTTPEDMALRYLATIQ
ALALGTRHIIETMNQNGYNIDTMM
ASGGGTRKNPIFVQEHANATGAMLLPEESEAMLL
GSAMMGTVAAAGVFESLPEAMAAMS
RIGHTVTPQTNKIKAYYDRKYRVFQMYHDHMR
YQALMQEGA"
gene      complement(245435..2463 /locus-tag="y0232"
88)
CDS       complement(245435..2463 /locus-tag="y0232"
88)

/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 20 to 310 of 317
are 58.76 pct identical to
residues 16 to 306 of 318 from
GenPept :
>gb|AAG54673.1|AE005211-8
(AE005211) putative permease
component of transport system,
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probably ribose specific
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
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/product="putative permease of ABC
transporter"
/protein-id="AAM83826.1"
/db-xref="GI:21956908"
/translation="MTWLNRTIPDDRIIRLQLLI
LIAVMLVFSLTILGQRFSLGNFQS
MSSQLPILGMLALGMGLTMLTGGINLSIIAGANA
CSLVMAAIIIVSHPGQAPAFLLALV
AGLLVAIVAIGTLNGVLISVIGVSPILATLGMTL
ITGLNILLSNGDVISGFFPVIQYI
GSGDIVGIPVAMILFLLVAAGLWVLEHTTLGRS
IYLVGSNEQATRFSGVNTHRVQIA
VYILSALLGWGAAILMMAKFNKAGYGESYLLV
TILASVLGGINPDGGFGRIIGLL
ALVVLQLESGLNLLGVSSYLTMAWGGVLILFI
ALQNRKA"
gene      complement(246390..2473
79)      /locus-tag="y0233"
CDS      complement(246390..2473
79)      /locus-tag="y0233"
          /function="transport; transport of
          small molecules; carbohydrates,
          organic acids, alcohols"
          /note="residues 6 to 321 of 329
          are 57.59 pct identical to
          residues 1 to 316 of 323 from
          GenPept :
          >gb|AAG54672.1|AE005211-7
          (AE005211) putative permease
          component of transport system,
          probably ribose specific
          [Escherichia coli O157:H7 EDL933]"
          /codon-start=1
          /transl-table=11
          /product="putative permease of ABC
          transporter"
          /protein-id="AAM83827.1"
          /db-xref="GI:21956909"
          /translation="MDKCLKRQLTGHHEFYLGLL
          VLLAIGLSVQSPEFLTLGNLTDV
          ATSYAILGILACGLFVVLIAGGDISFPVAITAIA
          QYVMASWVITQGGSFPLALVMAMA
          VGLLGLINGLLVYVWLVKVPAAITITATLNLFYGL
          LVYFTNGTWLYGFDPWFMTGINWF
          SFEGSDGYDYGLTLPLLCLAGTIIFTGVMMNYTR
          LGRQIFAMGSNKAASRLGINIFR
          LHLVYVYGMGILAGVAVVOAQISQSVAPNSLMG
          FELTVLAADVVLGGTSMGGRGSLT
          GTVLGVMLLAFLQNLGTLILLSVSSYWHTVFSGVII
          LVSISTAWNEKRKLLREH"
          /locus-tag="y0234"
gene      complement(247372..2488
68)      /locus-tag="y0234"
CDS      complement(247372..2488
68)      /locus-tag="y0234"
          /function="transport; transport of
          small molecules; carbohydrates,
          organic acids, alcohols"
          /note="residues 116 to 498 of 498

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are 61.19 pct identical to  
residues 9 to 392 of 392 from  
GenPept :  
>gb|AAG54671.1|AE005211-6  
(AE005211) putative ATP-binding  
component of transport system,  
probably ribose specific  
[Escherichia coli O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
/product="putative ATP-binding  
protein of ABC transporter"  
/protein-id="AAM83828.1"  
/db-xref="GI:21956910"  
/translation="MTQATAFITLENISKRFPGV  
LALDGVNLTLNKGEVHCLAGQNGC  
GKSTIIKVISGVYQPEKGASILIDGKLLHQLTPQ  
LSFYVYQVVIYQDLSLFPNLTVAE  
NIAVHRYLPGGDFWVKRKS MRERALAAMQVRGVT  
LDLDKKVEQLSIADRQLVAICRAI  
AADARLVIMDEPTASLTSQEVKGLLNVRDLKSQ  
GICVVFVSHRLDEVMEVADRISVM  
RDGKWVGWTQASELDSHELALMTGQRFTYRPLP  
PLAAKAAPLLEIRKLSRGEQFNNI  
DLTLHQGEIVSITGLLGAGRTELCLSLFGMTQPE  
SGEIFVAGEFVRFRRHNRDAIRHGI  
GYVSEDRLTQGLIMEQSIYDNTIVSVFDQLHTRS  
GLLDHSAALVNLVQDLNIVS  
DTALPVKTLSSGGNAQRIAIKQWVATQPRILILDS  
PTVGVDIANKEGIYHIAKALAEQG  
MAVLMICDEIPEAYYNHVRVLVMRKGELIAEFYP  
HQCTEQQIAEVVNG"

gene complement(249072..2501 /locus-tag="y0235"  
30)  
CDS complement(249072..2501 /locus-tag="y0235"  
30)

/function="transport; transport of  
small molecules; carbohydrates,  
organic acids, alcohols"  
/note="residues 25 to 350 of 352  
are 53.37 pct identical to  
residues 5 to 327 of 328 from  
GenPept :  
>gb|AAG54669.1|AE005211-4  
(AE005211) putative periplasmic  
binding protein, probable  
substrate ribose [Escherichia coli  
O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
/product="putative periplasmic  
binding protein of ABC  
transporter"  
/protein-id="AAM83829.1"  
/db-xref="GI:21956911"  
/translation="MQHNKISYLATVPLPERKQE  
GIAMKFNLALLNVCIVSACMLFTT  
QTLAAEKKHEIAVAVKVTGIPWFTRMVEGVNEAA  
KKLNVNAYQVGPA TPDPAAQQQVKVI  
EDLIAKNVDIAIIVVENDAKVLEPVLKKAQEKGV  
VLTHESPDQRIGQWDVETIDSEKY  
AQANMDELAKAMGNKGGYAIYVGS LTVPLHNAWA

gene 250774..251775

CDS 250774..251775

DYAIKYQKEKYPEMFVTPRLPVA  
ENIDKSYSTTLDLMKTYPQMKGIIGFSLGPIGA  
GQAVAKKRAKDQIAVVGIAMPAQA  
APYLMRGDIKKALLWDPKADGFAVVEIANQLLNG  
QKVTEDLTIDGLGKADVDSKNGVI  
RFNKILEVTKDNAKTLGF"  
/gene="ddg"  
/locus-tag="y0236"  
/gene="ddg"  
/locus-tag="y0236"  
/function="putative factor"  
/note="residues 25 to 333 of 333  
are 66.66 pct identical to  
residues 20 to 327 of 328 from E.  
coli K12 : B2378; residues 28 to  
333 of 333 are 66.66 pct identical  
to residues 1 to 305 of 306 from  
GenPept : >emb|CAD07638.1|  
(AL627274) putative  
acyltransferase [Salmonella  
enterica subsp. enterica serovar  
Typhi]"  
/codon-start=1  
/transl-table=11  
/product="putative heat shock  
protein"  
/protein-id="AAM83830.1"  
/db-xref="GI:21956912"  
/translation="MSEDMYRYRVMSLCVTHSHL  
THNDRVHMIKPQKFHISLLHPRYW  
LTWFGLVFLFLLVQLPYPLLNKLVGNLGRSTSMRF  
LKRVRSIARRNLELCFPDMDKQVL  
EQTIIGNFESLGMGLETTGMMAWFSDDTRIQRWFS  
VSGLENLKRAQQGKRGVLVIGVHF  
MSLELGGRVMGQCQPMAMYPHNNKVMELVQTW  
GMRMSNKAMLDRRDLRGMVRALKQ  
GEAVWFAPDQDYGRGSVFAPLFAVEHAATTSGT  
FMLARLAKPALLPLVLLRKKKEGRG  
YDLLIQPALEDYPIDDEIAAASYMNKVIEKEIMR  
APEQYLWLHRRFKTRPIGEPISLY"  
/locus-tag="y0237"  
/locus-tag="y0237"  
/note="residues 186 to 247 of 431  
are 26.15 pct identical to  
residues 515 to 579 of 865 from  
GenPept : >dbj|BAB73440.1|  
(AP003587) ORF-ID:a111741 probable  
proteinase [Nostoc sp. PCC 7120]"  
/codon-start=1  
/transl-table=11  
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/protein-id="AAM83831.1"  
/db-xref="GI:21956913"  
/translation="MKGKRAVGVVGITAHFILWF  
NRSNVALIPFFEGPSIMKSLILL  
ALLIPASVTANTLSVEPKDTKPALIDSLSATFAI  
DKIAMLKKEKGANESNLYLPFEQT  
KDGLAILFGDINQDGKIDALVPFTWEGLNGLDQE  
IPSNDSYSYAIYLDQDDQGWKQVG  
QIPTGTFTTTDNTLLTNIEDGVIYEIMPRMTDD  
DPQPQQWVLRHAHPEKDNLLVP IPT  
PQPLANALTNLNLSKRPLTRNALVTAFGEPINIG

gene 251819..253114

CDS 251819..253114

DNYFLVDGDCVGHDPWKYYQYPGA  
 AFNVSQNDNSVGVSHFIGIPDNLISVLGDLTITQ  
 KTSAHQLIKALSQNSDFTVSRST  
 DLRTDLGQSSPYDDANDIFALRLPYIAGFEAW  
 AKKNEAREVPNDDEADTFTRQFYF  
 TTTIGVAPIQNSPTRLMFYFLGDKMVALSVIYDD  
 GQVCI"

gene complement(253332..2550 /locus-tag="y0238"  
 02)  
 CDS complement(253332..2550 /locus-tag="y0238"  
 02)

/note="residues 8 to 554 of 556  
 are 75.13 pct identical to  
 residues 1 to 547 of 549 from E.  
 coli K12 : B4065; residues 5 to  
 555 of 556 are 74.95 pct identical  
 to residues 13 to 563 of 563 from  
 GenPept : >emb|CAD09253.1|  
 (AL627282) putative  
 sodium/hydrogen exchanger family  
 protein [Salmonella enterica  
 subsp. enterica serovar Typhi]"  
 /codon-start=1  
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 /product="hypothetical protein"  
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 /db-xref="GI:21956915"  
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 GALLAWPNFGLHVNFDPELFLVLFIPPLLFADGW  
 KTPREFIHHGREILGLALALVLV  
 TIVGIGYLIYWMVPGIPLVAFAALAVLSPTDAV  
 ALSGIVGKGRIKFSIMGVLEGEAL  
 MNDASGLVALKFAIAVAMGTMIFTVSGATLEFLK  
 VAIGGLLAGVAITWLYKSLRIMS  
 RWSGDDPATQIVLVLFFFASYLVAEHLGVSGIL  
 AAVAAGMTISQSGIIRNAPLAMRL  
 RADSVWSMLEFVFNGMVFIILLGLQLPGILETSIT  
 QAEIDPTIQTWNLFADVAIIYGAL  
 LLLRFGWLWSMKKISKRVLTKRPLQFSYDTTREL  
 WVASFAGVRGAILLAGVLSIPLFL  
 SDGSAFFSRYQLVFIATGVILLSVIIGVIALPPL  
 LRGVVVADKKSASREIIRLARAAMA  
 EVAIVSLNKMEERLMTSSEENIDSELLKEVSSRV  
 IGTLLRRRTGSKDEVENILLIENLE  
 RRFRLTALRAERGELYHLRATQKISNETLQKLLH  
 DLDLLEALLIEKG"

gene complement(255330..2566 /locus-tag="y0239"  
 85)  
 CDS complement(255330..2566 /locus-tag="y0239"  
 85)

/note="residues 4 to 451 of 451  
 are 85.04 pct identical to  
 residues 2 to 449 of 449 from E.  
 coli K12 : B4064; residues 9 to  
 451 of 451 are 87.35 pct identical  
 to residues 13 to 455 of 455 from  
 GenPept :  
 >gb|AAG58013.1|AE005518-7  
 (AE005518) 24223 gene product  
 [Escherichia coli O157:H7 EDL933]"  
 /codon-start=1

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/transl-table=11
/product="putative transporter"
/protein-id="AAM83833.1"
/db-xref="GI:21956916"
/translation="MSSSNPQAQPKGTLDAFFKL
SERGSNVROEVLAGLTTFLAMVYS
VIVVPSMLKGAGFPPTAVFVATCLVAGLSLLMG
LWANLPMAGCAISLTAFTAFSLV
LGQQISIPVALGAVFLMGVLFITISVTGIRSWIL
RNLPMGVAHGTGIGIGLFLLLIAA
NGVGLVIKNPIEGLFVALGAFTSFPVIMTLGLA
VIFGLEKLKRVPGGILLVIVAIISVI
GLIFDPVSVTYQGLFAMPSLADANGDSLIFSOLDIM
GALQPVVLPVSVLALVMTAVFDATG
TIRAVAGQANLLDKDQIISGGKALTDSVSSIF
AGLVGAAPAAVYIESAAGTAAGK
TGLTATVVGILFLLILFSLSYLVPAYATAPAL
MYVGLLMLSNVSKLDFEDFVDAMS
GLLCVFIIVLTCTNIVTGIMLGFSSLVIGRVCSGE
WRKLVNVTVIIAVALVAFYAGGWA I"
/locus-tag="y0240"
/locus-tag="y0240"
/notes="residues 7 to 66 of 67 are
38.33 pct identical to residues 26
to 85 of 86 from GenPept :
>gb|AAG54551.1|AE005201-4
(AE005201) damage-inducible
protein J [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative DNA-damage
inducible protein"
/protein-id="AAM83834.1"
/db-xref="GI:21956917"
/translation="MANAKALGLDLSTVIRMVVN
RLAVNAELPIDLLQPNQETLQAIR
DLENGVEVYRVDSDALKRDLGW"
/locus-tag="y0241"
/locus-tag="y0241"
/notes="residues 2 to 27 of 27 are
57.69 pct identical to residues 73
to 98 of 98 from GenPept :
>gb|AAF96231.1| (AE004370)
conserved hypothetical protein
[Vibrio cholerae]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83835.1"
/db-xref="GI:21956918"
/translation="MPDLLLIYQRTDSEIKLYRV
GSHSDLF"
/locus-tag="y0242"
/locus-tag="y0242"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"

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gene	257139..257342
CDS	257139..257342
gene	257698..257781
CDS	257698..257781
gene	complement (257961..258815)
CDS	complement (257961..258815)

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/note="residues 22 to 256 of 284
are 72.34 pct identical to
residues 8 to 242 of 255 from E.
coli K12 : B0933; residues 16 to
260 of 284 are 72.24 pct identical
to residues 11 to 255 of 274 from
GenPept :
>gb|AAG06830.1|AE004765-3
(AE004765) probable ATP-binding
component of ABC transporter
[Pseudomonas aeruginosa]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
component of a transport system of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83836.1"
/db-xref="GI:21956919"
/translation="MASGLSTKIRRSAMTTLTHI
PQGTPTITLESIGKRYGNRTVLDNL
QLRITAGQFVAVVGRSGCGKSTLLRLLAGLEAAS
DGTLLSGNALLSHAKDETRLMFOE
ARLLPWKKVIDNVGLGLRGHWREALQVLDIVGL
ADRANEWPAALSGGQKQKQVALARA
LIHRPRLLLDEPLGALDALTRIEMQGLIERLWQ
QHGFVLLVTHDVSEIALADRVL
LIEEGRIGLDLAIDLPRPRKGSAKLAALAEAVL
ERVLSPPQGIEASRGQIKASRQGT ATSRRVAN"
gene complement(258773..2595
70) /gene="ssuC"
CDS complement(258773..2595
70) /locus-tag="y0243"
/locus-tag="y0243"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/note="residues 1 to 260 of 265
are 79.61 pct identical to
residues 15 to 274 of 278 from E.
coli K12 : B0934; residues 2 to
264 of 265 are 80.98 pct identical
to residues 1 to 262 of 262 from
GenPept :
>gb|AAG06831.1|AE004765-4
(AE004765) probable permease of
ABC transporter [Pseudomonas
aeruginosa]"
/codon-start=1
/transl-table=11
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system permease protein of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83837.1"
/db-xref="GI:21956920"
/translation="MMTISAQRILHRLAPWILPV
ALVVGWQVAVEAGWLSNRILPAPS
AVVTAFWALTKSGELWQHLTISSWRALIGFSIGG
SIGVLGVITGLSRWGERLINSV
QMIRNVPHLALIPVLVWFGIDESAKIFLVALGT

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LFPIYLNTYHGKINIDSGLLEMAR
SYGLSGFRLLTQVVLPGALPSIMVGVRFALGFMM
LTLIVAEITISANSIGIGYLMANARE
FLQTDVVVVAIVLYALLGKLADGSAQLLERVWLR
WHPAYQQKSGEAQ"
gene      complement(259579..2607 /locus-tag="y0244"
27)
CDS       complement(259579..2607 /locus-tag="y0244"
27)

/note="residues 1 to 382 of 382
are 78.79 pct identical to
residues 1 to 381 of 381 from E.
coli K12 : B0935; residues 1 to
382 of 382 are 81.93 pct identical
to residues 1 to 382 of 382 from
GenPept :
>gb|AAF81710.1|AF250869-2
(AF250869) sulfonate monooxygenase
[Buttiauxella sp. PNB5]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83838.1"
/db-xref="GI:21956921"
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SEGARAVDYSYLQQAADRLGF
GGVLIPTGRSCEDSWLVAASLIPVTQRLKFLVAL
RPGIISPTLAARQAATLDRLSNGR
ALFNLVTGGDPEELAAGEHLNHTERYEASAEFT
HVWRKVLGETVDFAGKHIQVKA
KLLFPPVQHPRPPLYFGGSSAAQDLAAEQVELY
LTWGEPPQVKEKIEEVRAKAAK
GRTVRFGRHLHVIVRETTEAWRAANRLIANLDD
KTIADAQQAFAGFDSVGQORMAAL
HGGKKDNLEISPNLWAGVGLVRGGAGTALVGDGP
TVAQRIQEIADLGIDTFVFSGYPH
LEEAYRVSELLFPHLDLATTELPTRPATQPQGE
VVANIYVPQKVSQS"
gene      complement(260746..2618
82)
CDS       complement(260746..2618
82)

/locus-tag="y0245"
/gene="ssuA"

/locus-tag="y0245"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/note="residues 18 to 333 of 378
are 73.10 pct identical to
residues 17 to 331 of 333 from E.
coli K12 : B0936; residues 18 to
333 of 378 are 73.41 pct identical
to residues 17 to 331 of 333 from
GenPept :
>gb|AAG55421.1|AE005283-8
(AE005283) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="solute-binding
periplasmic protein of aliphatic

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sulfonates, ABC transporter"
/protein-id="AAM83839.1"
/db-xref="GI:21956922"
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AMAAIITLAFNTNTVIAQDNAPAQF
RIGYQKGSVNLVLAKTHQLLEKRFDPDTQISWIEF
PAGPQMLEALNVNSIDLGSTGDIP
PIFAQAAGADLLYVGMEPPKPKAEVILVPENSAI
NSVAELKGHKVAFQKSSSHNLLL
QALQKAGLKFTDIQPVYLTADARAFAAQGNVDA
WVIWDPYYSALLQGQIRVLIDGS
QLNQTGSFYLASRPYTEANGPFIIQQVLEVLTDQAD
ALTLSDRASITLLANAMGLEPAV
IASYLDHRPPTAIQPLSQATVAAQQORTADLFFAN
RLLPVKVDISQRVWQAPAGQLSSKP
PSSKPPSSSKPSSSNQSSPQLPTDQPSIAQTSIE
QSSTAKSQTK"
gene      complement(261897..2624 /locus-tag="y0246"
78)
CDS       complement(261897..2624 /locus-tag="y0246"
78)

/note="residues 1 to 175 of 193
are 61.14 pct identical to
residues 1 to 175 of 191 from E.
coli K12 : B0937; residues 1 to
175 of 193 are 61.71 pct identical
to residues 1 to 175 of 191 from
GenPept : >dbj|BAB34443.1|
(AP002553) NAD(P)H-dependent FMN
reductase [Escherichia coli
O157:H7]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83840.1"
/db-xref="GI:21956923"
/translation="MRVISLAGSPRTPSRSALL
NLSQHWLQQQNVVEIPYTLHDFQA
DDLRLANFNSPDVSAFVAQLATADGLLIATPIYK
ASFSGALKTLLDLLPERALDHKVV
LPLATGSGSIGHMLAVDYALKPVLTALKAQEVVLHG
VFVDDSQVVFHGEQVTVSTSATTR
LEEALSFYALGRRKPLASNAVSSSLVQQTAA"
gene      262949..263650
CDS       262949..263650
/locus-tag="y0247"
/function="enzyme"
/note="residues 9 to 225 of 233
are 34.10 pct identical to
residues 11 to 222 of 224 from
GenPept : >gb|AAB85318.1|
(AE000859) deoxyribose-phosphate
aldolase [Methanothermobacter
thermautotrophicus]"
/codon-start=1
/transl-table=11
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deoxyribose-phosphate aldolase"
/protein-id="AAM83841.1"
/db-xref="GI:21956924"
/translation="MIDFNDRQVAKAIQFTNVN
ADLTREGVIKHLNICLEYQFDAM
IAPCWVYLAKDVLKSGVRRVATTNFPQANDTTA

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MKVAIVRELAKEGADEFDFPPNPG
FLLGGLDELYFNELKEVTHIAHDLGMKVKAMLEF
GFITEAMKIKATRYAYEAGIDWV
KQSSGWGKGGCAATVEDVQLLKANIQAPCRVKVS
GKVNITLEKMKEMFLAGAEVLVTSS
GPELVKGLTGDINAY"
gene      263804..264736      /locus-tag="y0248"
CDS       263804..264736      /locus-tag="y0248"
                        /function="enzyme; degradation of
                        small molecules; Carbon compounds"
                        /note="residues 4 to 299 of 310
                        are 39.26 pct identical to
                        residues 5 to 301 of 308 from
                        GenPept :
                        >gb|AAG05338.1|AE004621-9
                        (AE004621) ribokinase [Pseudomonas
                        aeruginosa]"
                        /codon-start=1
                        /transl-table=11
                        /product="putative ribokinase"
                        /protein-id="AAM83842.1"
                        /db-xref="GI:21956926"
                        /translation="MMSVFILGSYAKALVMTTDR
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                        AVQAVRLGAEVAYAGVVGDDTFGHEFVGLMQEEG
                        VNIDALTIISGELFTGAGLIVKDKE
                        ARNVIVVDMGANKLFTPALVDSALSQ LKQSNVVL
                        TQLEIPL ETARYGLQRAKEFGKIT
                        ILNPAPARDLRGLDLSAIDYLTPNETEARVALGL
                        PPDDPRSNREIANLLLETGCQYVV
                        MTLGESGSAVFGRNDTQEIIPCCIIDVVDNSGAGD
                        SFNAALAVALDEGLPISEAVLFAN
                        ATAAALCCMDWETVPSYRYREDVD AFMRSITVKEE
                        "
gene      264742..265245      /locus-tag="y0249"
CDS       264742..265245      /locus-tag="y0249"
                        /function="putative transport;
                        transport of small molecules;
                        carbohydrates, organic acids,
                        alcohols"
                        /note="residues 1 to 135 of 167
                        are 34.04 pct identical to
                        residues 1 to 139 of 139 from
                        GenPept : >gb|AAC22159.1| (U32732)
                        high affinity ribose transport
                        protein (rbsD) [Haemophilus
                        influenzae Rd]"
                        /codon-start=1
                        /transl-table=11
                        /product="putative inner membrane
                        permease"
                        /protein-id="AAM83843.1"
                        /db-xref="GI:21956927"
                        /translation="MRPDRI LHP ELAALATLGH
                        TDIILVTDAGFP IIPPQAKRIDLGF
                        WPGTVDVLHILRVLRKEIFVEEVRFASEVRDCHP
                        QLYRDVQTLTYTSGGAEFQAASHET
                        LCHDLAHQAKVVIRSGSFNPWANFALVASTDPFA
                        WFTDESGVKPLPAYVARRQRILDN VPELNA"
gene      complement(265407..2663 48) /locus-tag="y0250"
CDS       complement(265407..2663 /locus-tag="y0250"

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/function="regulator"
/note="residues 54 to 306 of 313
are 23.57 pct identical to
residues 51 to 302 of 307 from
GenPept :
>gb|AAG06959.1|AE004778-3
(AE004778) transcriptional
regulator MmsR [Pseudomonas
aeruginosa]"
/codon-start=1
/transl-table=11
/product="putative AraC-like
regulator"
/protein-id="AAM83844.1"
/db-xref="GI:21956928"
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LVNRYILRAGHIRAADNFHVRQSVAGHELIFCL
NGSGFIRLENNLHEVKKGNLAWLP
VRWFPEHFPNKQEPWEILWLRIDGAKLNNIMQIL
DVAQQPVFEFTSPETITDIYHRLF
DLMQSHTLVADACHDVLCSQLIYTLLENRSFDT
KSPVISHRGLGRLIYQIHSYHND
WDIDKFMQYQVSKSOLFRLFQETFNQSPPLRWL
NYRLSQARLLVETEETISRIAGL
VGYNDPLHFHSRDFHRSVGLSPDFRRQERQLDND
RHD"
/locus-tag="y0251"
/locus-tag="y0251"
/note="residues 18 to 370 of 376
are 43.94 pct identical to
residues 13 to 359 of 362 from
GenPept : >dbj|BAB49039.1|
(AP002998) hypothetical protein
[Mesorhizobium loti]"
/codon-start=1
/transl-table=11
/product="putative oxidoreductase"
/protein-id="AAM83845.1"
/db-xref="GI:21956929"
/translation="MDTLISQLEHATQVLPKRR
DYRIGIIGAGFIVEHCHLVAYQKA
GFVPYGITSKESQNHRLAETFAIKKVYETWQDM
VCDPQIDIIDIAVPFHQLEIVRF
ICESNSAAKHIGILCQKPLAMSLKDGREIVRLS
QQSGIPIAVNSNMRYDPSMRALKY
ILENQLIGDPVIASIDMRAIPDWQAFLLQYKKLE
LYAMAIHHIDAFRFLFGDPVKVTA
VCRDPRTTTFEHDGITQYTFQYANGLIATSLDD
VWAWPGEPCAKNYINNRVEGSDG
LAEGDFGWHRREFYCGSTLKLASRNHPGQNIAP
KWERQWFPDAFIGTMANLMCAIEE
NRPEPISAEADNLGTLACIEACYLSIQQERTVYLN
EILLENAK"
/locus-tag="y0252"
/locus-tag="y0252"
/note="endonuclease motif;
residues 1 to 298 of 299 are 51.48
pct identical to residues 1 to 303
of 304 from GenPept :
>dbj|BAB49038.1| (AP002998)

```

gene	266543..267673
CDS	266543..267673
gene	267670..268569
CDS	267670..268569

```

unknown protein [Mesorhizobium
loti]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83846.1"
/db-xref="GI:21956930"
/translation="MINVGIFTGYYPYTLSTGID
KIKQAGMGCVQLDLEFTDIDLRG
RITKEKAHQVRNAFRANIPVAISAYTNLVHPD
PVKRAENIAAVKEILAHARHFGTP
YVISETGTNTSDSDWLYDPKNSTEEAYQEKAIA
KELATFAYEHNNAVLFVENYVNNII
GSVGQVARLMQVEVHPGLGLALDPTNYFDDKNID
AIDETLHNIFNVLESRIKIAHAKD
CKKTDATAEKFGGAAEHNSFRGAGSVLPAAGL
GALNYPLYVELLAQKHPNIPLIIE
HVDEEDIPRAKRFVDEVLMATGS"
/locus-tag="y0253"
/locus-tag="y0253"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83847.1"
/db-xref="GI:21956931"
/translation="MDWIQDNSEMYLAGDWTQT
GLTG"
gene      complement(268916..2697
CDS      10) /locus-tag="y0254"
complement(268916..2697 /locus-tag="y0254"
CDS      10)

/Note="residues 42 to 145 of 264
are 31.77 pct identical to
residues 163 to 258 of 325 from
GenPept : >emb|CAB12673.1|
(Z99108) similar to iron(III)
dicitrate transport permease
[Bacillus subtilis]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83848.1"
/db-xref="GI:21956932"
/translation="MCTAIAIAYGTENIPPETAYE
IGMLFFKVIELDTSTGGYKYRED
RSEEDIDFIEVSLSDLKNELKNKNATSFRRYNES
EKSNIYWTASFGFSTSDFGGFYHFD
AQCALSKNGKEKFIIEFIKEFSSKNNSYSGIVYNP
DNVADGFYYAEGGNFVQIYQYENP
MFFEKETGGMVEGQERYKNTMLRMVYPNVNINH
HLDIIIGNVSLKEWISSDEKHGTL
EGLNNDLWLWTVEDTKLDEVNKYLGEAGVLISWK
PPTIKKAPRKLK"
gene      complement(269719..2742 /locus-tag="y0255"
CDS      63)
complement(269719..2742 /locus-tag="y0255"
CDS      63)

/Note="Rhs element associated;
residues 89 to 1396 of 1514 are
33.53 pct identical to residues
112 to 1362 of 1517 from GenPept :
>emb|CAD18288.1| (AL646083)

```

putative Rhs-related transmembrane  
 protein [Ralstonia solanacearum]"  
 /codon-start=1  
 /transl-table=11  
 /product="Rhs-like core protein"  
 /protein-id="AAM83849.1"  
 /db-xref="GI:21956933"  
 /translation="MFMTVAQSIGTGYGAAGQS  
 ALRQTALGQQSPARTDYQVSNPNV  
 GN1ARASDSSLNVAESQQFNTLVTAGFGMQAIAA  
 GVAGGYVGAKIGNKLGHGIARALN  
 FNQVATEGESPAHLGHP1AHQKDKDGVWGAIGGI  
 LLGAAAAALVVVTFGTGLVIVIAAA  
 AAAAAGLIGGIAAATGAALGQYGDNKGVIAEGSAN  
 VFFEQGPVARVGDKIQCSDHPSSP  
 PPMIAEGAKTVFANQKQIARLGHRTTCGGINAG  
 CGSLAITQETAIVVEADSRNPYL  
 RWSAVILSFLPIQKKFEQGRSLKKPPNTAVNAT  
 HNCPTGSDPDMVSGDYLQWVPVI  
 DIAGVLPVRLQRTYRSGDYFTVSGCFGHKWADSW  
 SQHLVVHEDNIDYIDEEGVGLSFF  
 TPENKVQAVNLNLRYLGERHGLRVLFRDSTQ  
 QTLHFNQQQQQRYLSAITDRKGN  
 RIDFRYQQGELISVEHSDGYVLEIDSRGRTIHAV  
 ELVTEKQRKQLQSTFSERGVLVQ  
 CQSFQYGTLSHEYDPKGYMVRWRDSDSDVAVRY  
 DISGRVVALKTSTGFFADHF1YHD  
 KERYTIYRDGEGGETGYHYNENLLIKLVDPLGN  
 TTLTDWDLTKIKETDALGRITRF  
 IYNERGDLTAVILPDETRTEYEYNPSGVVTAFTS  
 SAGDSWQYQYDRQGLLRQVTPSG  
 QTMSEFRYKKGVLKRI1AEDQVWRYHYDHHGCL  
 STIIDPKGNSTAVTLDVLGRLEFSH  
 QNALGELTRYTHSDAHASPAGSVTKMVPDQVEQ  
 AIAYDSEKRIAALTDGAGKTTRYE  
 YGGFDLLTGLIRPDGQRLTFGYDTLTRLNQVTNA  
 SGDTYRYTRDRAGQV1SETDFTGR  
 TVHYQYDAVGRRIGARYPDQRLVRWHYSMQDQVL  
 AQQTWHCDALSSSTLVGTVSYGYDG  
 AGRLLSATNADAVVEFDYDEAGQLVAERLNGREV  
 RHQWDALNGTPVARQVGELGLTFV  
 YGAQGELTRLQLAGHQPLQLQHDRLGRETVRESA  
 AGFIQACNYTPSGLLAHQAAGRNS  
 ALFQQQLIAPESPALHGSAVNRSWQYDRAYNVVG  
 MDDGRWGKTYQYDRNDQVVRADF  
 GGFLLPQEQFSYDVNQNLRHRCCLPRGAQAVLAQ  
 ASQQQQAGRVVVKRGSQRYDAAG  
 RLVEKRSQKDGYPQLWRYRWNEQDQLSELITPT  
 GARWRYGYDAFGRIRKLRLVVDTP  
 PLNEMDAPSTGPATASLAGAYLWSGDQLIEEVF  
 VYADGTIVAYEQGIHWLYAPGGLTP  
 MARYAQCKLHYVVDHLGTPRELLNEQGKVVWAS  
 RLSTWGQAE1WRQAANEEDRVSCN  
 LRFAGQYADAESGLHYNFRFYDGETGQYLCPDP  
 IGLEGLNPGYVHNVPVSWVDPLG  
 LATCPMREVNGTK1FGKGQKDGTPGHDQFSEVIA  
 NKLAMSGKFKEVYLNRSYNFANGK  
 GISGRRPD1MAVDMNGKVHAIELAS  
 KTDMRKFP1SLRTRNQDAMKNLPSIDRGSVIVL  
 EHQYNSKIKNALDNLISGI"

gene

complement (274302..2747  
 24) /locus-tag="y0256"

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CDS      complement(274302..2747 /locus-tag="y0256"
24)

        /note="residues 1 to 137 of 140
        are 36.49 pct identical to
        residues 4 to 140 of 143 from
        GenPept : >emb|CAD18289.1|
        (AL646083) conserved hypothetical
        protein [Ralstonia solanacearum]"
        /codon-start=1
        /transl-table=11
        /product="hypothetical"
        /protein-id="AAM83850.1"
        /db-xref="GI:21956934"
        /translation="MYFNEGSLELPEAWRDMTV
        NVLTSSLDETVGLSFTVSRDTPPW
        GMGFHEFFDREIGSLSRQLNHYQLLHQDTGEVNN
        HPSVTAEFCWSSEQGRIHQMLTLV
        DIAPRVLILTATMVGELTPQQKEHITAIVQTLQI
        NARS"

gene      complement(274727..2768 /locus-tag="y0257"
29)

CDS      complement(274727..2768 /locus-tag="y0257"
29)

        /note="Rhs element associated;
        residues 77 to 696 of 700 are
        46.91 pct identical to residues 3
        to 633 of 633 from GenPept :
        >gb|AAG54902.1|AE005236-3
        (AE005236) Z0707 gene product
        [Escherichia coli O157:H7 EDL933]"
        /codon-start=1
        /transl-table=11
        /product="VgrG-like protein"
        /protein-id="AAM83851.1"
        /db-xref="GI:21956935"
        /translation="MSGAQMTMAGGIGDAVGGT
        AGKRINQAAEVAKTALDAKAKVLD
        GGVTPILNLAAGGAGAGLPDSAAAALTRLVKPSPG
        LQFTLTITASLPPQTFVAVDFTLSE
        MLSSPFVLNVGLASADPAVDFAAVLDEDAITLFIW
        REGVLQRSITGMVASFEQDGTGFH
        QTRYSMVIRPALWRTSLRNRARIFQQASVEEIIIT
        TLLKENGINDFAFGFRHPHPVREF
        CVQYQESDFDFIQRLTAEEGIFYFSEFSAGKNTV
        VYADDVGSLEPKGASLPYNPNVAAQ
        AQELSITTFTRSAQVRPAMVOLKDYTFKNPNWAA
        AFSEQSGELQNQRPDYEHFDPPGR
        FKDAQHGQDFTTRYRLDALRNDANLQGGASNDFTL
        QPGQLFSLYNHPRGDLNHAQQLLG
        VQHSQKQMQALEQASGDQGTVLNFHFSFIPHTQT
        WRPTPLAKPAMDGPQIAMVVGPPG
        EEIYCDEYGRIRLQFLWDRYQGSNDNSSCWIRVT
        QPWAGQGWGMLAIPRIGQEVVVDF
        LHGDPPDQPIVTGRTYHANNIPPGSLPASKTQMAF
        RSKTHQGEYGNEMRFEDAKGGEGL
        FMHAQKDMSTTVKDNQTTTVEKGNQTVTVEKGDR
        TVTVATGNETTDITQGSLLTETIKV
        RRSCTANFIQVKAEGDAPGTQLYTATEQIKFVVVG
        KSSITLNPDSIILQFSGSTSITLN
        AANIDAIAPLINLNKDKG"

gene      complement(276826..2769 /locus-tag="y0258"
24)

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CDS complement(276826..276924) /locus-tag="y0258"

/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83852.1"  
/db-xref="GI:21956936"  
/translation="MFAHDKANNKTADKTGTVT  
PTHIVSFEAAQP"

gene complement(276946..277122) /locus-tag="y0259"

CDS complement(276946..277122) /locus-tag="y0259"

/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83853.1"  
/db-xref="GI:21956937"  
/translation="MQTELNREIPLEELLRLQ LAV  
SADEHQFPASPVLIRKIDDRWNALL  
SRYHHLLTQQTNSAR"

gene 277204..277692 /locus-tag="y0260"

CDS 277204..277692 /locus-tag="y0260"

/function="regulator"  
/note="residues 48 to 154 of 162  
are 33.64 pct identical to  
residues 6 to 108 of 112 from  
GenPept : >gb|AAF94621.1|  
(AE004224) transcriptional  
repressor RstR [Vibrio cholerae]"

/codon-start=1  
/transl-table=11  
/product="transcriptional  
repressor"  
/protein-id="AAM83854.1"  
/db-xref="GI:21956939"  
/translation="MHRITISNSIAIRCVFVFKS  
GLILEHMTDVIDEIMQTEEQRRR  
FGLRLKELRKQQHKTKQEVATRIGLQLSQYNKYE  
SGMHIPPADKLITLAELLVTSIDY  
LLLGSSNETSSIRNTRLERFKALSQCQPEEQET  
VIKLIDAVIVKHVESALQVPDPE KK"

gene 277774..277998 /locus-tag="y0261"

CDS 277774..277998 /locus-tag="y0261"

/note="residues 15 to 68 of 74 are  
42.59 pct identical to residues 35  
to 88 of 132 from GenPept :  
>gb|AAA97244.1| (U14003) ORF-f132  
[Escherichia coli]"

/codon-start=1  
/transl-table=11  
/product="hypothetical"  
/protein-id="AAM83855.1"  
/db-xref="GI:21956940"  
/translation="MAKAHSTSGTGINKTPKTER  
YYTVGYVPQGRKNPPPAINLKGK  
WLEALGFFSGQPVLTITVEHGRVLIQPEIKI"

gene complement(277977..278174) /locus-tag="y0262"

CDS complement(277977..278174) /locus-tag="y0262"

/codon-start=1

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/translation="MSHSPDRDSSPLSCIQAII
LLYFKYCAGRKSCINNIGFVDNEF
RDIIVHNTVENNIPIHIFISG"
/locus-tag="y0263"
/locus-tag="y0263"
/notes="residues 15 to 63 of 63 are
34.69 pct identical to residues
177 to 224 of 243 from GenPept :
>gb|AAG55242.1|AE005267-7
(AE005267) arginine 3rd transport
system periplasmic binding protein
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83857.1"
/db-xref="GI:21956942"
/translation="MQDLRPAQYLKYNINVMAWI
QDNGLSLSGEWLTQTGLTGQPLA
ISVMAGKVIIQFQKNMMLL"
/locus-tag="y0264"
/locus-tag="y0264"
/notes="residues 17 to 157 of 161
are 25.97 pct identical to
residues 29 to 169 of 192 from
GenPept : >gb|AAC12984.1|
(AF020713) unknown [Bacteriophage
SPBc2]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83858.1"
/db-xref="GI:21956943"
/translation="MKNPCQNCENIDLSDIKSV
EKTILGYSFPEAFVSHYLSFNGGVP
LRANWACDDGCEPLEIAAFKPFKYHKMTNDNPNS
LIDGCYNEMIRKNVIPSNIIPFGN
DWGGNFFCLNKDDSVVFYAIDSFDEPVSMKSNH
DVLQKKLTSSFEFFINGLVEEDDL E"
/locus-tag="y0265"
/locus-tag="y0265"
/notes="Rhs element associated;
residues 8 to 326 of 456 are 44.23
pct identical to residues 957 to
1250 of 1354 from GenPept :
>emb|CAD08751.1| (AL627266)
Rhs-family protein [Salmonella
enterica subsp. enterica serovar
Typh1]"
/codon-start=1
/transl-table=11
/product="rhsD protein"
/protein-id="AAM83859.1"
/db-xref="GI:21956944"

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gene 278074..278265

CDS 278074..278265

gene complement(278315..278800)

CDS complement(278315..278800)

gene complement(278802..280172)

CDS complement(278802..280172)

```

/translation="MAADLLPRQGDWIRKFSFDT
AGELSMATDFIRGEQQYRYDAEGR
LTDSRERHQLSVAEDFAYDNADNLLNLRKLPFDT
VDPLYDTPVANNRLTQWQHRYRFEY
DAWGNMTTRHAGGRMQHFAYDDNRLLRAGTGFP
LGEHDSHYRYDALGRRIHKSVTIK
RGAEKTTTROTDFIWQGLRLLQEQTDTGNATYIID
PNESYTPPLARVDQRHGETESQVYY
FHTDINGTPLDVTDEGEKHRWSGKYHAWGVTRQ
NVSDPRQSTVSFRAQPLRYPGQYS
DDEITGLHNTFRYYDPEIGRFSTQDPFGLAGGIN
LYQYGPNNPLTWIDPWGAWFGVDVF
TGSPLDFPVKGSQNLNIVEITMQGARGRDFTEAFK
LAGISKADATGYTWHLNDFDPVS
GKTTMQLVTTSAHEATFPHAGSVSQFEKHFNLP
QSYGSADAVAISHSKGWLKGRIFK ALRSGC"
gene      complement(280200..2830 /locus-tag="y0266"
91)
CDS       complement(280200..2830 /locus-tag="y0266"
91)

/note="Rhs element associated;
residues 10 to 960 of 963 are
37.73 pct identical to residues 1
to 934 of 1364 from GenPept :
>gb|AAL19248.1| (AE008708)
putative Rhs-family protein
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="Rhs-like protein"
/protein-id="AAM83860.1"
/db-xref="GI:21956945"
/translation="MRRGPGRPAMFEARVDDKL
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AYAASIVLTGGATLVATGFIVGMGVTTLGVVAGG
LIRSVGEKIGSMCHHDVGGQITTS
KNVKVNSKRAAHVELSTVACKDDSAIQRMAEGSS
NIFINSKAARLEDKTTCTDAVVDS
ASSNVTFGGGRVQYLDIKREISDEMRLSEKLF
VAGLAGGIFGAQAQACFGGLKCLS
KIALGEMAGAAAAGYGLEKGVGAIAGYFGYPVDVI
SGQKLLTGEGDDTDFILPGIFPLH
WSRIYRSENNHHVVALGQGSVLWERSLRKEDDSI
VYQNDEGREIVFPLIKRGERYFSP
TEHIWLARTERTYAISSPFETCFIFEAFSEAGV
AKLASLEDLNGHALYFSYDDIGQL
KKISITTSYGYVYCYQYKGRLVSVACVKGTPGTL
VRYQYNEQHQLVSVTNREGQITRQ
FGYHGHLLINKLADVRLGLECTRYTADIGGTPRITH
SATNLGEQWQFDYDIDNQQTTLTD
LNTGQTACWGYNQAHLITDYRDFGKGKAYFDYND
LNMPVRVVLAGERTLVLVYDALAR
PIQITDPLKRETHIDYHRNSLRVVRQYPDGQVM
KGEYDRTRGLLENAPDGGVTLVH
YPGASSLPERITNAVGAQTHLWGERHGQLTEHTD
CSGKLTREYDIDGHLLTVIDAEN
HSTHYSYNRLGQPTGIRYADGRKEQLRYNAQGLV
EQFTDPVGRQLHWRYNLRGQPVSF
TDRLQREYRYRYDCHGQMIELDNANGGQYHFRWS
SGGQLVEEQYPDNLVRRYRYGESG
MLMALETTAPTVDLTVSRQVDFDYDAGGRMTQR
LTGMSATRYDWDIMDRLLLAERP

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TAVGEQAGIVGHGVRLAYDKAGHLLTESGDLGAV
TYQWDLPHHLLAALTLPDGTLSWL
RYGAGHVS AIRHGDTLISEFSRDNLHREVSR TQG
ILTYRQDYDAMGRRL"
gene      complement(283057..2835 /locus-tag="y0267"
15)
CDS       complement(283057..2835 /locus-tag="y0267"
15)
/note="residues 9 to 144 of 152
are 35.71 pct identical to
residues 5 to 144 of 148 from
GenPept : >gb|AAL19247.1|
(AE008708) putative cytoplasmic
protein [Salmonella typhimurium
LT2]"
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/transl-table=11
/product="hypothetical"
/protein-id="AAM83861.1"
/db-xref="GI:21956946"
/translation="MPENNINTYCIQEGTLECPE
GFTDRTVNLFMKGKFGAFAFNIA
RDVPEAEHVLSDYVQORQIGILKDNLKKYEVKKHQ
QIDVGAQHIPGEYVEATYMAETRR
VMQRQVAIQVGDHMMIFTATNASPFNPQQQATWE
QWHSFAPWAREAGHV"
gene      complement(283521..2859 /locus-tag="y0268"
23)
CDS       complement(283521..2859 /locus-tag="y0268"
23)
/note="VgrG-like protein (Rhs
element associated); residues 169
to 792 of 800 are 44.06 pct
identical to residues 3 to 674 of
713 from GenPept : >gb|AAC62387.1|
(AF044506) VgrG protein
[Escherichia coli]"
/codon-start=1
/transl-table=11
/product="VgrG-like protein"
/protein-id="AAM83862.1"
/db-xref="GI:21956947"
/translation="MFAHDKANNKAAKTGTVT
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IGDAVGGTAGKRINQAAEVAKTALDAKAKVLDGG
VPTINIVATGPAPTIVSGAQMTMA
GGIGDAVGGTAGKRINQAAEVAKTALDAKAKVLD
GGVTPMNLAAAGGAGAGLPDSAAAA
ISRLVKQPSGLQFTLTASLPPQTFVAVDFTLSE
MLSSPFVLNVGLASADPAVDFAAV
LDEATLFIWREGVLQRSITGMVASFEQDGTGFH
QTRYSMVIRPALWRTSLRRNARIF
QQASVEEIIITLLKENGINDAFGFRHHPVPREF
CVQYQESDFDFIQRLTAEEGIFY
FEFSAGKNTVVYADDVGS LPKGASLPYNPNVAAQ
AQELSIITFTRSAQVRPAMVQLKD
YTFKNPNWAAAFSEQSGELQNRPDYEHDFDPGR
FKDAQHGQDFTRYRLDALRNDANL
GQGA S NDFTLQPGQLFSLYNHPRGDLNHAWQLLG
IQHSGKQMQALEQASGDQGTVLFN
HFSFIPHTQTWRPPTLAKPAMDGPQIAMVVGPPG
EEIYCDEYGRIRLQFLWDYRQSN

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		DNSSCWIRVTQPWAGQGWMGLAIPRIGQEVVVDF LHGDPDQPIVTRGRTHANNIPPGS LPASKTQMAFRSKTHKGEYNEMRFEDAKGGEGL FMHAQKDMTTMVLNRKTDVTDQH SEHIGQDQSVTVVRNQSNNTIQNDRRVEVTRDQQT EVGNDYQLVVKGEKKEFVTKIRYT EVHDETLTVTKSIKIHAKQGDISTPNAGITI THDGAIVLQGGYIRLAADMIDLNP EE"
gene	complement(285945..287257)	/locus-tag="y0269"
		/note="disrupted by frameshift"
		/pseudo
gene	287229..287591	/locus-tag="y0270"
CDS	287229..287591	/locus-tag="y0270"
		/note="residues 19 to 79 of 120 are 34.84 pct identical to residues 53 to 114 of 311 from GenPept : >gb AAC17095.1  (AC004482) hypothetical protein [Arabidopsis thaliana]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83863.1"
		/db-xref="GI:21956948"
		/translation="MMICCGVSLMQTHPLIVFLP FKQQEDVMTTINTICLNASVSMRS VSIQSCVSIQSVWQTEFTEQTAREWVVGFIKDKA VRHLAAILNLEADIEGVGAHIGQFT GVDQPOLRPRTAEAGAR"
gene	complement(287382..290842)	/locus-tag="y0271"
		/note="disrupted by frameshift"
		/pseudo
gene	complement(290946..292352)	/locus-tag="y0272"
CDS	complement(290946..292352)	/locus-tag="y0272"
		/note="residues 213 to 462 of 468 are 53.33 pct identical to residues 8 to 259 of 264 from GenPept : >gb AAG54520.1 AE005198-1 (AE005198) 20251 gene product [Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83864.1"
		/db-xref="GI:21956950"
		/translation="MSLVRHMDITSQHPWHVLLQ APLSPEQTAQALADDDPOWEYIDG QMKVLGSLAHATLNIIDDIIQQAMALLSQKSKDFR LVVHLRLTLQHGGQFDEMLMLMSL LTEYVQLFWTTAWPONPLHKRRFAQQIILKRFDSA SSFSQRADEAQRENVQGLLAHLA QVWHSREPLAKEVDALRSRYARPPERVIEAVAS DEPLSSNTLAAAMAATPVSPSLAI DNTSDRAWRQTLKMDLLSEQOPDAAIGFRLRR HAVWGALTAPPMQSGDRTPLAUV SADRTADYLARLANADLPLHQVEQSLTLAPYWL DGHVLSAQIALQLGYDAVAQAIRD

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                                ELSVFLARIPALKTLFFDTMTPLSLSESAAWLQQ
                                DANHQGRSRTIEQDEIWQCQQQQG
                                LEALQMINRQPQQSEPRDRFYHQLLSAQLFEKA
                                GLTALAQQHYHSLLLVGQQQLQLE
                                WEPALIALLTEKQQLKP"
gene      complement(292340..2930 /locus-tag="y0273"
35)
CDS       complement(292340..2930 /locus-tag="y0273"
35)
                                /note="residues 36 to 231 of 231
                                are 50.00 pct identical to
                                residues 47 to 244 of 247 from
                                GenPept :
                                >gb|AAG54522.1|AE005198-3
                                (AE005198) Z0253 gene product
                                [Escherichia coli O157:H7 EDL933]"
                                /codon-start=1
                                /transl-table=11
                                /product="hypothetical"
                                /protein-id="AAM83865.1"
                                /db-xref="GI:21956951"
                                /translation="MPAMNTWLLISSLLFSGGHT
                                DAFWTMGLPPPVAEKEEAGTLALV
                                MRCRSENSALVRDCYDKALSPVNAVDEKRVNAG
                                PAWQRAMNOEKGRTDHSTAFLVTE
                                GEGSNPMVLITTPAIGMPPRPVLMMLSCIDNITR
                                LQIALVGPKESVTLIIDKAGII
                                DKTRLDAQWFLRENGYLLESSRGLAGIDEIKRLM
                                SAETLTIEGANGAFFRLTFTLSQL
                                TPALKPLRNACHW"
gene      complement(293023..2938 /locus-tag="y0274"
20)
CDS       complement(293023..2938 /locus-tag="y0274"
20)
                                /note="residues 194 to 260 of 265
                                are 29.57 pct identical to
                                residues 454 to 524 of 530 from
                                GenPept : >gb|AAF96031.1|
                                (AE004353) sigma-54 dependent
                                transcriptional regulator [Vibrio
                                cholerae]"
                                /codon-start=1
                                /transl-table=11
                                /product="hypothetical"
                                /protein-id="AAM83866.1"
                                /db-xref="GI:21956952"
                                /translation="MRQRLKSVLALLDNDSTEQI
                                IHRFLTINHHRQRFSAIMVSMFNA
                                SEGRLCDYHQPDGGMNVALKLDANIEDVNHPLVR
                                VLRNGFPFVWGSLYQGVRIEDDDF
                                RSFIALPTRCGLYALPLFDVHGACGVIASFSE
                                NIERFADTRGIFSIYCHIFQHLRN
                                KLQEMDQLRSQFNQIRTVFKEQRQREKQLDELLV
                                SLSTSDTHALPGISQDYKIDSLT
                                TAVETFECAVLTQRQRLYGNDKSRIAASGLSLR
                                ALTYKLAKYRCQL"
gene      complement(293817..2964 /gene="c1pB"
20)
                                /locus-tag="y0275"
CDS       complement(293817..2964 /gene="c1pB"
20)
                                /locus-tag="y0275"

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/function="putative enzyme;
degradation of proteins, peptides,
glyco"
/note="residues 153 to 857 of 867
are 40.22 pct identical to
residues 133 to 849 of 857 from E.
coli K12 : B2592; residues 1 to
866 of 867 are 67.25 pct identical
to residues 1 to 910 of 923 from
GenPept :
>gb|AAG54523.1|AE005198-4
(AE005198) putative protease
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="heat shock protein"
/protein-id="AAM83867.1"
/db-xref="GI:21956953"
/translation="MIQIDLPTLVNRLNPIARHS
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QAITQAYPSFSPLLVENVLQDSWLL
ASTEMEHSQLRSGVMILLTLLSPSRYLVPNTANRL
LSPINRELLRQNFANWTADSAETP
RAEKGAEEAGNGAEINGDSLLARYASNMTQARNG
ELDPVLCRDTEIDLMDILCRRRK
NNPIVVGEEAGVGKSALIEGLALRIVDNQVPEKLR
NSELMTLDLGAQAGAAVKGEFEK
RFKGIMAEIAQSTTPIILFIDEAHTLIGAGNQQG
GLDISNLLKPALARGEKLTIAATT
WSEYKYYFEKDAALSRRFQLVKVSEPSAQEATII
MRGLRTVYEQAHGVLIDDEALQAA
AVLSDRYISGRQLPDKAIDVLTAAARVAINLTS
APROVSALKNELYHQCMEIEMLER
EQRLSLSRDPDERLSVLQQQRIEIEQQLIALNTGW
EKQQHLVQQIIALRAVLLAQEESA
TDEQVVNLTALSDELERLQQHQLTVSPHVDKSI
AAVIAEWTVGPLNRLSQSELAVVT
ELPSYLGQQIKGQETAHCLHQHLLTARADLRP
GRPMGAFFLLVGPSPGVGKTETVLQI
ADLLYGGQYLTINMSEFOEKHTVSRIGSPPG
YVGYGEGGVLTETARQKFPYSVLL
DEVEKAHPDVNLNLFYQAFDKGELADGEGRIIDCK
NIVFFLTSLNGYQTIIVDHADEPAL
LNERLYPELSAFFKPALLARMEVVPYPLPLGMETL
QIIHGKLNRLDTLLRQRFADVV
IEPEVIDEILLRATRAENGARMLESIIDGALLPP
VSLLLQKVAAGTAISHIRIAVEG
NVFTAQVEGAI"

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gene      complement(296431..2971 /locus-tag="y0276"
98)
CDS       complement(296431..2971 /locus-tag="y0276"
98)

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/function="putative membrane"
/note="residues 20 to 254 of 255
are 62.55 pct identical to
residues 18 to 252 of 253 from
GenPept :
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(AE005198) Z0255 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1

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/transl-table=11
/product="putative membrane
protein"
/protein-id="AAM83868.1"
/db-xref="GI:21956954"
/translation="MKTDVAVTNTNTPFAAEAVTS
HRQYQLPLRGESLNAMIDTATPLL
GMVLRLLKDMENQALPDQLYQQVVTDIRAIEQYLQ
TKGYEFGAIIISFRYVLCFIDETA
LGHGWNTQNGWLQQSLLVHFHNETWGGEKVVYLL
ERLMGEFPKRYQDLLEFIYLCFCCLG
YRGRYKVTSSQNGDDFERLFRRLHHQLQQLRGDAP
PTVLYQGGGRLNSRYHLSKRLLTIK
HLLWGGVSLLVVIYLFYAIHLHTQSQDILQQLNN
LLS"

gene      complement(297198..2985
44)
CDS       complement(297198..2985
44)

/locus-tag="y0277"

/note="residues 3 to 446 of 448
are 53.60 pct identical to
residues 4 to 442 of 443 from
GenPept :
>gb|AAG54525.1|AE005198-6
(AE005198) 20256 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83869.1"
/db-xref="GI:21956955"
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QQQQRHNDYQLQRRIIALQGYRYG
FSSILNQELLKLGRIGLTVASGNMADGTVFIDIP
YQDYSKPLDVLNCDNDAASRDIYL
ALPMLNDAINVAGQQQAPGTLRYREHSDDVDR
LHTEGGDVSQVLVAQLAPRLMQGS
EDLSAYSVLPLCRVKEKRPDGSILDEEFIPTCT
TLVSSTQLKGFMDVEGTLVERAQ
LLAKRIGSPGQQGIADVAEFMMLQVFNRTQPLET
HLAHQAAILHPEAFYHQLVQTCGEL
RTFTDESRLAGTFPVYNHNDLDSFQPLFLAMRQ
ALSTVLTTPRAISIQLHMQAHGIRV
ATINDSDLLRSADFVLAVRAQIPQEQLRRQFVQQ
TKITSLEKIRDLVSVQLFPGVPLVA
LSAAPRQLPHYSGYTYFMLDLQSPVWKEIQQSNA
IAFHVSGDFPDLDMQFWAIRSS"

gene      complement(298547..2990
92)
CDS       complement(298547..2990
92)

/locus-tag="y0278"

/note="residues 3 to 181 of 181
are 46.92 pct identical to
residues 2 to 174 of 174 from
GenPept :
>gb|AAG54526.1|AE005198-7
(AE005198) 20257 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83870.1"

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/db-xref="GI:21956956"
/translation="MNNARGYLLTALCVVFLLS
GCSGAWKATKVGKVVMDPDIPVG
QATDQPSVRLTLLSDPDTPNPEKGEAVPTEIVV
VYLSKNSKLLAADYDQLSSDALEK
TLGKNYIDHQEYTLPLDQFKALDPKLEEKNSYL
GVIAHYADANRSEWKKIIKIGIG
HNYQVLVHVRSDNDVLRKEEE"
/locus-tag="y0279"
gene      complement(299092..3004
08)
CDS       complement(299092..3004
08)

/note="residues 2 to 438
are 45.47 pct identical to
residues 10 to 432 of 433 from
GenPept :
>gb|AAG54527.1|AE005198-8
(AE005198) Z0258 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83871.1"
/db-xref="GI:21956957"
/translation="MDKKQPTLSLRVNSDKLES
GKQASSLFHTQGGSVGSDGSHHWS
IQDQGGNISPSQFAIEWRDGSEFCLRLNGSLNIN
HSMLTNPSGQFVRLQGGDEMTLGNL
VIKSHISRSAADMDPLMVSPESLVSSSYNPMDA
MMEGEPLASPHHQDSDRLAATVSH
NFSHDLPLRVLETESTLTQGHDAVISDADHSLQDD
RYRNPLFSSPLSDTPKDSAMDQAF
IDLQISTFLNGKQAGGKPEGLNNQMEQHHVAIT
PLMRGFDAQLPIRNSQEAHDFLEE
AGKTLKATIEGLLALQRSQHGLRDKHLRPIDNPF
LRLNMDYDTTLNLMFADQKSPVHL
SAPAAVAESLDNLRLLHQANQQAITQALNTMLEA
FSPERLLTRFTHYLRNSNERQEQDS
AWAWDMYKNYINELASSRQGGFEKLFGEVYEQAY
DRALRQGMKDSE"
/locus-tag="y0280"
gene      complement(300534..3016
31)
CDS       complement(300534..3016
31)

/note="residues 44 to 363 of 365
are 57.89 pct identical to
residues 37 to 358 of 360 from
GenPept :
>gb|AAG54528.1|AE005198-9
(AE005198) Z0259 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83872.1"
/db-xref="GI:21956958"
/translation="MLRMAGTDRSTCTDVSVVED
VSGVENVNGVEARPEGQALDVSRV
NFFQLVELLNQLAVAWQGAAPVATPANEAIRFKS
TASLAFPTRDVIALDTSARGQFEL
EVSVFLGLHGSQSLPGYYLDSLAWEDAQNENRLT
DFMNVFNHRLTLHLHQIWRKYRY"

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		ICFDNGGDDAFSQRMFSLVGLGSEVVRNKLQINH SKMLAYAGLLASPGRAPEVICSLV SHCFNLPDITLHSWQLRKVDIAPSQQNRLGTRVK VRGKKYDEKSVLGVNFSIGSRVAD RSGKFLLCINKLTREQFLSFLPNGANYASLVMFV AFIMRDQFAWDLRLGLAEQQVGGM VLGTEQNSLLGWTSLGDPEQKPSVTIGVME"
gene	complement(301586..302458)	/locus-tag="y0281"
CDS	complement(301586..302458)	/locus-tag="y0281"
		/note="residues 46 to 290 of 290 are 55.51 pct identical to residues 345 to 589 of 589 from GenPept : >gb AAF96024.1  (AE004353) hypothetical protein [Vibrio cholerae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83873.1" /db-xref="GI:21956959" /translation="MRFPAEWPFLKGNVEPPLGG LKKGVSLNRTSRSWIKRSKIWGSV HRGHGREYTSFESFHHQIEHSQEKALYRLRVK NSLFRKGFEHYISFVRSDSEKLV AEENVSVSLTCTNRELPLSLRVGDINQLSTDSPS FATFRNITRPSVPLYPVLDGGLHW SLLSNMSLNYMSLLDKDALKQLLHTYDFPSLHNR QSRASQKKLDAIQRIETQPIDRL FRGLPVRLQTTLWLEQGAFSSEGELYLFSTVLA RFFSLYASVNAFHLLKVINLNDQE CYEWPVQTGQHALM" /locus-tag="y0282" /locus-tag="y0282" /function="IS and transposon related functions" /note="IS1661 transposase; residues 56 to 224 of 226 are 39.64 pct identical to residues 1 to 167 of 173 from GenPept : >emb CAA63546.1  (X92970) orfA [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83874.1" /db-xref="GI:21956960" /translation="MNFSHVGNKVRSLASVRS DGGSSQTRCTPGHDPGALNPRSWI FLSMIWRFGSMKHPFSTRLAQVHYLSGKATLRE TARQFSVGKSPLTRWIRAFRRQGE AGLEHHLSTRITYPEFRLCVVRYMMANRCSAADAS AHFNIPNETIIQNWMKRYREGGKE ALNPSKTGPTMPKDKYEHDSKPFSEMTHAELEKE LEYLRAENAYLKKRKALREKALR EQKKKPE" /note="insertion element; partial" /insertion-seq="IS1661" /locus-tag="y0283" /locus-tag="y0283" /function="IS and transposon related functions"
gene	302218..302895	
CDS	302218..302895	
		/note="residues 46 to 290 of 290 are 55.51 pct identical to residues 345 to 589 of 589 from GenPept : >gb AAF96024.1  (AE004353) hypothetical protein [Vibrio cholerae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83873.1" /db-xref="GI:21956959" /translation="MRFPAEWPFLKGNVEPPLGG LKKGVSLNRTSRSWIKRSKIWGSV HRGHGREYTSFESFHHQIEHSQEKALYRLRVK NSLFRKGFEHYISFVRSDSEKLV AEENVSVSLTCTNRELPLSLRVGDINQLSTDSPS FATFRNITRPSVPLYPVLDGGLHW SLLSNMSLNYMSLLDKDALKQLLHTYDFPSLHNR QSRASQKKLDAIQRIETQPIDRL FRGLPVRLQTTLWLEQGAFSSEGELYLFSTVLA RFFSLYASVNAFHLLKVINLNDQE CYEWPVQTGQHALM" /locus-tag="y0282" /locus-tag="y0282" /function="IS and transposon related functions" /note="IS1661 transposase; residues 56 to 224 of 226 are 39.64 pct identical to residues 1 to 167 of 173 from GenPept : >emb CAA63546.1  (X92970) orfA [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83874.1" /db-xref="GI:21956960" /translation="MNFSHVGNKVRSLASVRS DGGSSQTRCTPGHDPGALNPRSWI FLSMIWRFGSMKHPFSTRLAQVHYLSGKATLRE TARQFSVGKSPLTRWIRAFRRQGE AGLEHHLSTRITYPEFRLCVVRYMMANRCSAADAS AHFNIPNETIIQNWMKRYREGGKE ALNPSKTGPTMPKDKYEHDSKPFSEMTHAELEKE LEYLRAENAYLKKRKALREKALR EQKKKPE" /note="insertion element; partial" /insertion-seq="IS1661" /locus-tag="y0283" /locus-tag="y0283" /function="IS and transposon related functions"
repeat-region	302324..303509	
gene	302949..303569	
CDS	302949..303569	

repeat-region 303510..305463  
 gene 303596..304618  
 CDS 303596..304618

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/note="IS1661 transposase;
residues 3 to 187 of 206 are 45.74
pct identical to residues 24 to
207 of 283 from GenPept :
>gb|AAB18535.2| (U00039) orfB in
IS150 [Escherichia coli]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83875.1"
/db-xref="GI:21956961"
/translation="MARSTYYHASKPDGVIDDY
ADAVKAIGALSRRHQAQRYGYRRMT
VALRKEGFTLNHKTVRKLMNQHGLLSIRRKYYR
SYRADGGRASDNLLARNFTSEISG
LKWCTDVTFRVGAQKLYLSVIQDLFNNEIISWH
MSERAALILCTKILEKALKVKGRK
EGLMLHSDQGWHYRTPMWRSMLEAGICNERCNS
DPHPTPEIRSRG"
/note="insertion element"
/insertion-seq="IS100"
/locus-tag="y0284"
/locus-tag="y0284"
/function="IS and transposon
related functions"
/note="IS100; orfA; residues 1 to
340 of 340 are 100.00 pct
identical to residues 1 to 340 of
340 from GenPept : >gb|AAC13168.1|
(AF053947) putative transposase
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83876.1"
/db-xref="GI:21956962"
/translation="MVFETVMEIKILHKQGMSS
RAIARELGISRNTVKRYLQAKSEP
PKYTPRPAPAVASLLDEYRDYIRQIADAHFYKIPA
TVIAREIRDQGYRGGMITLRAFIR
SLSPQEQEPAVRFETEPGRQMOVDWGIMNRGS
PLHVFVAVLGYSRMLYIEFTDNMR
YDTLETCRHNARFFGGVPREVLYDNMKTIVLQR
DAYQTGQHRFHPSLWQFGKEMGFS
PRLCRFPFAQTGKGVVERMVQYTRNSFYIPLMTRL
RPMGITVDVETANRHGLRWLHDVA
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VHLDENLVNFDKHLHPLSIYDS FCRGVA"
/locus-tag="y0285"
/locus-tag="y0285"
/function="IS and transposon
related functions"
/note="IS100; orfB; residues 1 to
260 of 260 are 100.00 pct
identical to residues 1 to 260 of
260 from GenPept : >gb|AAC69770.1|
(AF074612) putative transposase
[Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83877.1"

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gene 304615..305397  
 CDS 304615..305397

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/db-xref="GI:21956963"
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SLISAAPALSQQAVDQEQWSYMDFL
EHLHHEKLARHQRKQAMYTRMAAFPAVKTFEY
DFTFATGAPQKQLQSLRSLSFIER
NENIVLLGPSGVGKTHLIAIAMGYEAVRAGIKVRF
TTAADLLQLSTAQRQGRYKTTLQ
RGVMAPRLLIIEIGYLPFSQEEAKLFFQVIAKR
YEKAMILTSLNLPFGQWDQTFAGD
AALTSAMLDRILHSHSHVQIKGESYRLRQKRKAG
VIAEANPE"
repeat-region complement(305463..3056 /note="insertion element; partial"
63) /insertion-seq="IS1541a"
gene complement(305910..3080 /locus-tag="y0286"
24)
CDS complement(305910..3080 /locus-tag="y0286"
24)

/function="putative membrane;
transport of small molecules;
cations"
/note="similar to colicin V
secretion ATP-binding protein
CvaB; residues 1 to 698 of 704 are
57.16 pct identical to residues 1
to 698 of 698 from GenPept :
>gb|AAL08400.1| (AF063590) MceG
[Klebsiella pneumoniae]"
/codon-start=1
/transl-table=11
/product="putative secretion
ATPase"
/protein-id="AAM83878.1"
/db-xref="GI:21956965"
/translation="MNDIHFEIKNRLNFSFRKK
VPQVLQTEAAECGLACLVMTCRIH
GMDIDLFLNLRQRFGISSHGATLALLINISAQLKF
KTRALSLDLDELRLQKTKPCILHWD
MSHFVVLVAVKGRFIIHDPAFGRRTVSLSEMSQ
HFTGVALELWPNSEFTROKSRTRL
SLLSLMRNISGLPGFLTNIKFCLSMVEAINLLP
VGTQLVMDHVIIAEDYDLLALICI
GLLFFILFRFTFLSMLRSWTSILVMGSLVDVQWKAG
LFDHLLKLPLAYFEKRLGDIQSR
FGSLDIIRSTLTNNVNGIIDGLMSIGVFIMMFL
YGGWLWVVLGFTAMYMLRLATY
NQYRQASEEQIVKNKASSHFMETLYGISTLKAL
GLAATRSQFWLNLNIDTTNANIRL
TKLDMFFGGVNTLIGTIDQVVLWLWLGASMVIDGQ
MTLGMFVAFNAYRGQFSDRATNLI
NMVLQLRMLALHSEIRIADIVFTETEKEQTPRQLL
SPNQPAVFERNIAFQYDNLKPEI
FSDLNIHVEAGESVAITGPSGIGKTTLMKVIAGL
LTPSQGHILIDGLDITTVGLNNYR
DCIACVLQDDKLFAGSIADNIAFSFVNVKDEQRIL
SCANHCNIHKEIMHMPMGYETLIS
ELGGSLSGGQKQRLLIARALYRQPSLLFLDEATS
HLDLANEAHINNAIASLKITRIFI
AHRPSTIASAQRIINLEKQNVS"
gene complement(308017..3093 /locus-tag="y0287"
33)
CDS complement(308017..3093 /locus-tag="y0287"

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gene	309522..309761	/function="putative membrane; transport of small molecules; cations" /note="similar to colicin V secretion protein CvaA; residues 14 to 438 of 438 are 47.05 pct identical to residues 1 to 424 of 424 from GenPept : >emb CAC21493.1  (AJ278866) MchE protein [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative secretion permease" /protein-id="AAM83879.1" /db-xref="GI:21956966" /translation="MMGITERGMSSNQIFRRDAV EYIRTKWLKGALLTSGYSTTFIAA LCAIFLVLLITLIITYGTYTRRINVNGEVISQPHF INIFSPQQGFITKKWVEVGDIVRK GQHLHYQIDVSRITTFSGNVLSNLSLEAINNQLSQID SIINNTQKNKELTLLNLRQQLAQY QKAHKKSQELVDNAGKGMDMRTMASYGYTQRQ GLITKDQLTNQRSLEYQQQNAFQS LNTQLIQESLQIAKLESEISTRASDFDNDISQYL FQKGDCLKRQLAEVDASGMLLINSF SDGKIENMSVTQGGQMVNVNDSLVLQTPSDNPYYC LVLWVPNNSVPIYINTGDKVNIRYD AFFPEKFGQFPGRISISNVFVSQQEIASYNIAP RLPNGGLIEPYKIVALDDIHFR YQSKPLMLSNGLKANVTFLLEKRPLYQWMLSPFY DIKKSVTGPVNE"
CDS	309522..309761	/locus-tag="y0288" /locus-tag="y0288" /note="residues 12 to 72 of 79 are 31.14 pct identical to residues 383 to 440 of 657 from GenPept : >gb AAB18717.1  (U38906) ORF42 [Bacteriophage rlt]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83880.1" /db-xref="GI:21956967" /translation="MKELTQTEVMEVSGAGIVSD AGKVLGSGFGALIDAGASIFGIKP NASATIGKIGESIGSAFDAGISGVKQFFGLSAPQ Q" /locus-tag="y0289" /locus-tag="y0289" /note="residues 7 to 48 of 49 are 26.19 pct identical to residues 262 to 303 of 355 from GenPept : >gb AAF98228.1  (U64843) hypothetical protein K06C4.8 [Caenorhabditis elegans]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83881.1" /db-xref="GI:21956968"
gene	309936..310085	
CDS	309936..310085	

		/translation="MKIAYRTIRFINLWIYAVFY SEFFGFELSHYLSADMIFFGDYE FILYH" /locus-tag="y0290"
gene	complement(310351..310512)	
CDS	complement(310351..310512)	/locus-tag="y0290"
		/note="residues 4 to 40 of 53 are 37.83 pct identical to residues 159 to 195 of 195 from GenPept : >emb CAC09571.1  (AJ298983) S-receptor kinase (SRK) [Fagus sylvatica]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83882.1" /db-xref="GI:21956969" /translation="MACSDFACSEIAHADTDSVM ATIKATPAVVVLRKQQLCIKPP HQDVNELSQ" /locus-tag="y0291" /locus-tag="y0291" /note="residues 10 to 30 of 143 are 66.66 pct identical to residues 1017 to 1037 of 1263 from GenPept : >gb AAG31016.1  (AY007367) tospovirus resistance protein D [Lycopersicon esculentum]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83883.1" /db-xref="GI:21956970" /translation="MAHLNARFDDKEGLFEGASQ SGTLILRNISARACQVNAMPVIS FEGAVGQQLAVFRKVPGRMQEPVLSPTVAAGA EVAVQLRWVASDAFDGNNCVTPEK VVVTLGGTLRLPFGRMCAASGDTEFFSQAPVG PATNEVQ" /locus-tag="y0292" /function="putative enzyme; biosynthesis of cofactors, carriers: Menaquinone, ubiquinone" /note="menaquinone biosynthesis; residues 1 to 161 of 161 are 87.57 pct identical to residues 1 to 161 of 161 from E. coli K12 : B3929" /codon-start=1 /transl-table=11 /product="2-heptaprenyl-1,4-naphth oquinone methyltransferase" /protein-id="AAM83884.1" /db-xref="GI:21956971" /translation="MKYDTSDLCDIYHEEVNVVE PLFSNFGRTSFGKITTVCED NGLFLDLEENGLRVLVVDDGGSVRRALINAEI
gene	310544..310975	
CDS	310544..310975	
gene	complement(311092..311577)	/gene="menG"
CDS	complement(311092..311577)	/locus-tag="y0292" /gene="menG"

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AELALKNEWEGIVVYGAVRQVDDL
AELDIGIQAMAAIPVGADEGVGESDIRVNFEGV
TFFSGDHLAYADNTGIILSEDPLDI E"
gene      complement(311719..3126 /gene="menA"
48)      /locus-tag="y0293"
CDS      complement(311719..3126 /gene="menA"
48)      /locus-tag="y0293"
          /function="enzyme; biosynthesis of
          cofactors, carriers: Menaquinone,
          ubiquinone"
          /note="1,4-dihydroxy-2-naphthoate
          --> dimethylmenaquinone; residues
          12 to 309 of 309 are 68.12 pct
          identical to residues 7 to 304 of
          308 from E. coli K12 : B3930;
          residues 12 to 309 of 309 are
          69.12 pct identical to residues 8
          to 305 of 309 from GenPept :
          >gb|AAL22930.1| (AE008891)
          1,4-dihydroxy-2-naphthoate
          octaprenyltransferase [Salmonella
          typhimurium LT2]"
          /codon-start=1
          /transl-table=11
          /product="1,4-dihydroxy-2-naphthoa
          te octaprenyltransferase"
          /protein-id="AAM83885.1"
          /db-xref="GI:21956972"
          /translation="MKRKMSLSINTSQTQAWLES
          LRPRTLPLAFASIVTGSALAVWLD
          SFKPAVALLALLTAGLLQILSNLANDYDGA VKGS
          DTEERIGPLRGMQKGIISHQMKV
          ALIITVILTIISGIALIAVACEKPSDILGFLLLG
          LMAIVAAITYTVGRKPYGYMGLGD
          ISVLVFFGWL SVAGTYYLQAGHFDIVMLPATAC
          GLLATAVLNINNRDIENDKANGK
          NTLAVRLGPVVARYYHALLIGAAIFCLALFSILH
          LHSWHGWIFLLAIPLLGKHALFVL
          RDPTAAGMRPMLQMKVKAALLTNILFAVGLVFS"
gene      complement(312872..3142 /gene="hslU"
03)      /locus-tag="y0294"
CDS      complement(312872..3142 /gene="hslU"
03)      /locus-tag="y0294"
          /function="factor; adaptations,
          atypical conditions"
          /note="homologous to chaperones;
          residues 1 to 443 of 443 are 90.29
          pct identical to residues 1 to 443
          of 443 from E. coli K12 : B3931"
          /codon-start=1
          /transl-table=11
          /product="heat shock protein,
          ATPase subunit"
          /protein-id="AAM83886.1"
          /db-xref="GI:21956973"
          /translation="MSEMTPREIVSELD SHIIGQ
          DKAKRAVAIALRNRWRRMQLNEL
          RHEVTPKNILMIGPTGVGKTEIARRLAKLANAPF

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IKVEATKFTEVGYGVGKEVDSSIIRD  
 LTDAAVKMVRHQSIKEMRYRAEELAEERILDLVLI  
 PPAKNNWGVDPDESQEPSATRQTFR  
 KKLREGQLDDKEIEIDLAAAPMGVEIMAPPGME  
 MTNQLQSMFQNIAGQKQKPRKIKI  
 KEALKLLIEEEAAKLVNPEELKQQAIDAVEQHGI  
 VFIDEIDKICKRGQTSGPSVREG  
 VQRDLLPLVEGCTVSTKHGMVKTIDHILFIASGAF  
 QVSSPSDLIPELQGRLPRIVELQA  
 LTDDFERILTEPSASLTEQYKALMATEGVTIEF  
 TREGIRKIAEAAQVNVERTENIGA  
 RRLHTVLERLMEDISYDASESSGQSITIDAEYVG  
 KHLDELVADEDLRSFIL"

gene	complement(314274..314798)	/gene="hslV"	
		/locus-tag="y0295"	
CDS	complement(314274..314798)	/gene="hslV"	
		/locus-tag="y0295"	
		/function="enzyme; degradation of proteins, peptides, glyco"	
		/note="residues 1 to 174 of 174 are 90.80 pct identical to residues 1 to 174 of 176 from E. coli K12 : B3932; residues 1 to 174 of 174 are 100.00 pct identical to residues 1 to 174 of 174 from GenPept : >emb CAC88971.1  (AJ414141) heat shock protein [Yersinia pestis]"	
		/codon-start=1	
		/transl-table=11	
		/product="heat shock protein, proteasome-related peptidase subunit"	
		/protein-id="AAM83887.1"	
		/db-xref="GI:21956974"	
		/translation="MTTIVSVRRDGHVVIGGDGQ VTLGNTVMKGNAKKVRRLYNNKVI AGFAGGTADAFTLFELFERKLEMHQHGLTKAAVE LAKDWRTRDRLRKLEALLAVADET ASLIITGNGDVVQPEDDLIAIGSGGPYAQSAARA LLENTELGARDIVEKSLSIAGDIC IYTNRFQTIEELTY"	
gene	complement(314898..315743)	/gene="ftsN"	
		/locus-tag="y0296"	
CDS	complement(314898..315743)	/gene="ftsN"	
		/locus-tag="y0296"	
		/function="phenotype; cell division"	
		/note="residues 1 to 281 of 281 are 49.68 pct identical to residues 1 to 319 of 319 from E. coli K12 : B3933; residues 1 to 281 of 281 are 51.38 pct identical to residues 1 to 324 of 324 from GenPept : >gb AAL22933.1  (AE008891) essential cell division protein [Salmonella typhimurium LT2]"	

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/codon-start=1
/transl-table=11
/product="essential cell division
protein"
/protein-id="AAM83888.1"
/db-xref="GI:21956975"
/translation="MAQRDYSRGRSGARRKSTS
RKKRSAPIVSKTVMALAVALLVVF
VGGLYFITHNKPGEPLPLPNHDFRTGNGLPPKPE
ERWRYIKELNRQIGVPMPTPEPSA
GGEVNAKTELTTNEQRQLLEQMADMRRQOPTQLSE
VPYNQGMQQVPRSAVTIKPPATSV
QPQPVTIPPQTITIPVQPAAPVTPPAAPVTQA
VTPPKVEKEKEKTQRMMVQCGSFK
AVDQAESIRAQLAFAGIESRITSGGGWNRVVLGP
YNSKAAADKALQRLQAGQSGCIP LSVGG"
gene      complement(315809..3168
37)      /gene="cytR"

CDS      complement(315809..3168
37)      /locus-tag="y0297"
          /gene="cytR"
          /locus-tag="y0297"
          /function="regulator; global
          regulatory functions"
          /note="residues 1 to 339 of 342
          are 71.38 pct identical to
          residues 1 to 339 of 341 from E.
          coli K12 : B3934"
          /codon-start=1
          /transl-table=11
          /product="regulator for deo
          operon, udp, cdd, tsx, nupC, and
          nupG"
          /protein-id="AAM83889.1"
          /db-xref="GI:21956976"
          /translation="MENKKEFTMTTMKDVAEMAG
          VSTATVSRALMNPKEKVSTVTRQKV
          EQAVLAVGYSPHALSRNIKRNESRTILVIVPDIS
          DPFFADVIQGIEHAAAQQGYLILI
          GDCAQQQTQERTFVNLIITKQIDGMLLLGSNLPF
          DASKEEQRNLPFMMVMAEFAPLE
          LPTVHIDNLTAAEAVNYLHELGHKRIACIAGPE
          SLPLSHYRLQGYIQALRRNGITVD
          NDYIIRGDFS YEAGAQSF AALMELPHPTAIFSH
          NDVMAVGAIWQAKQLGLRIPQDVS
          LVGFDDLKLSQFCDPPLTTVAQFRYIQGQAMLL
          LLEQLQGHSVQSGSRLLDTELIIR ESTAAPKH"
gene      complement(317190..3193
88)      /gene="priA"

CDS      complement(317190..3193
88)      /locus-tag="y0298"
          /gene="priA"
          /locus-tag="y0298"
          /function="factor; DNA -
          replication, repair,
          restriction/modification"
          /note="factor Y; putative
          helicase; residues 1 to 731 of 732
          are 73.08 pct identical to
          residues 1 to 731 of 732 from E.
          coli K12 : B3935; residues 1 to
          731 of 732 are 72.67 pct identical

```

to residues 1 to 731 of 732 from  
 GenPept : >gb|AAL22935.1|  
 (AE008891) primosomal protein N'  
 (= factor Y) directs replication  
 fork assembly at D-loops  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="primosomal protein N"  
 /protein-id="AAM83890.1"  
 /db-xref="GI:21956978"  
 /translation="MSVVQVALPVPLARTFDYRL  
 DSAMACPVVGARVSPVFGKRKAIG  
 IVVGLSDTSTFPLEQLKTIDAILDNHSLFPFSLW  
 RILCWATEYHYHPIGEVLPHALPI  
 LLRQGRFAQSAPLWQWVFVTEQGRATPPESLKRAP  
 KQQQALALLQKPVYRHQVNMAL  
 TESALQALRSKGLIDLRAQEATTDWRHSFSVLG  
 ERLRLNTEQATAVGAIRSEDNQFA  
 AWLLAGVTGSGKTEVYLSVLNILAQGRQALILV  
 PEIGLTPQTIARFRERFNAPVEVL  
 HSGLNDSERLSVWLRRSAGEAAIVIGTRSAFTF  
 FSRLGVIIIDEHDSSYKQQEGWR  
 YHARDLAVFRAREEGIPVMTATPALETLHNQV  
 MGKYRQLTLTKRAGSAKPAQAHL  
 DLKGLPLKVGLSQPLLQMKTHLQAGNQVILFLN  
 RRGYAPALLCHECGWIAECQRCDH  
 YYTLHQNHRLRCHHCDSQRVPVQPCPKGSGTHL  
 VSVGVGTEQLENELAPLFPETPIT  
 RIDRDTTSRKGSLQYLADVHQGGARILIGTQML  
 AKGHHFPDVTLLVALLDVGALFSA  
 DFRSAERFAQLYTQVSGRAGRAGKQGEVILQTHH  
 PEHPLQLILLQGGYDAFAKQALEE  
 RKSVFLPPYTSHIIVRSEDHNDQSSALFLQQLRN  
 LLEASPLKDEALWIMGPVPALQAK  
 RGGFRWQLLLQHPSRQLLQRLIKTSQPLISTLP  
 QARKVKWTIDVDPIDS"  
 /gene="rpmE"  
 /locus-tag="y0299"  
 /gene="rpmE"  
 /locus-tag="y0299"  
 /function="structural component;  
 ribosomal proteins - synthesis,  
 modification"  
 /note="residues 20 to 89 of 90 are  
 81.42 pct identical to residues 1  
 to 70 of 70 from E. coli K12 :  
 B3936"  
 /codon-start=1  
 /transl-table=11  
 /product="50S ribosomal subunit  
 protein L31"  
 /protein-id="AAM83891.1"  
 /db-xref="GI:21956979"  
 /translation="MWCLAEQGWATRPNIEVSM  
 KQGIHPKYEQVTAASCSGNGVIRIN  
 STVGHDLNLDVCGECHPFYTGKQRDVASGGRVDR  
 FNKRFSVPGAKK"

gene 319574..319846

CDS 319574..319846

gene complement(320371..320838) /locus-tag="y0300"

CDS complement(320371..320838) /locus-tag="y0300"

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/note="residues 13 to 140 of 155
are 65.62 pct identical to
residues 10 to 137 of 146 from E.
coli K12 : B3562; residues 5 to
150 of 155 are 57.53 pct identical
to residues 1 to 146 of 166 from
GenPept : >emb|CAD13669.1|
(AL646057) hypothetical
transmembrane protein [Ralstonia
solanacearum]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83892.1"
/db-xref="GI:21956980"
/translation="MDLNMNPNYAKPSAAFTAAS
WSALLGGFVIFLIGLWNADMQLNE
RGYYFAVLILGLFSAVSLQKTVRDKLEGLAITSI
YYGLCWVAFIVAVLLLCIGLWNAT
LALSEKGFYGVFTFFMTLFGAIAVQKNTRDSAMSS
DTEASLFLPKKVRDQLKAED"
gene      complement(321175..3214
92)      /gene="metJ"
CDS      complement(321175..3214
92)      /locus-tag="y0301"
          /gene="metJ"
          /locus-tag="y0301"
          /function="regulator; amino acid
          biosynthesis: Methionine"
          /note="residues 1 to 105 of 105
          are 89.52 pct identical to
          residues 1 to 105 of 105 from E.
          coli K12 : B3938; residues 1 to
          105 of 105 are 91.42 pct identical
          to residues 1 to 105 of 105 from
          GenPept : >gb|AAL22939.1|
          (AE008891) transcriptional
          repressor of all met genes but
          metF (MetJ family) [Salmonella
          typhimurium LT2]"
          /codon-start=1
          /transl-table=11
          /product="repressor of all met
          genes but metF"
          /protein-id="AAM83893.1"
          /db-xref="GI:21956981"
          /translation="MAEWNGEYVSPYAEHGKSK
          QVKKITVSIPLKVLKILTDERTR
          QVNNLRHATNSELCEAFLHAFTGQPLPNDEDLR
          KERSDEIPEAAKILMRELGVDPDT WEY"
gene      321789..323029      /locus-tag="y0302"
          /note="metB; disrupted by
          frameshift"
          /pseudo
gene      323032..325467      /gene="metL"
          /locus-tag="y0303"
CDS      323032..325467      /gene="metL"
          /locus-tag="y0303"
          /function="enzyme; amino acid
          biosynthesis: Methionine"
          /note="residues 8 to 811 of 811
          are 83.95 pct identical to

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residues 7 to 810 of 810 from E.  
 coli K12 : B3940; residues 8 to  
 811 of 811 are 83.95 pct identical  
 to residues 7 to 810 of 810 from  
 GenPept :  
 >gb|AAG59141.1|AE005625-4  
 (AE005625) aspartokinase II and  
 homoserine dehydrogenase II  
 [Escherichia coli O157:H7 EDL933]"  
 /codon-start=1  
 /transl-table=11  
 /product="aspartokinase II and  
 homoserine dehydrogenase II"  
 /protein-id="AAM83894.1"  
 /db-xref="GI:21956982"  
 /translation="MNATAVAAAATGRQLHKFGG  
 SSLADVKCYLRVANIMANYSHPGD  
 LMVVSAGSTTNQLISWLKLSQNDRLSAHQVQQS  
 LRRYQHDLINGLLPPEMAEPLISE  
 FIHDLERLAGLLDNKIDDDVIYAEVVGHGEIWSAR  
 LMSALLNKLMDDAVWLDARRFLRA  
 ERAAQPIDESRSYPLLQQLMAQHPHQLVVTGF  
 ISRNEAGETVLLGRNGSDYATQV  
 GALAGAERTIIVSDVAGVYSADPRKVKDACLLPL  
 LRLDEASELARLAAPVLHTRTLQP  
 VSGSDIDLQLRCSYQPEQGSTRIERVASGLGAK  
 IVTSHDDVCLIELQIASHHDFSLA  
 QKEIDLKRAQIKPLATGIHPDRNLLQCYTSE  
 VVNSALRVLEDAALPGKLSLREGI  
 ALVALVGAGVSKNPLHSHRFYQQLKDQPVFEVWQ  
 AEDGISMVAVLRLGPTHEHLIQGLH  
 QSLFRAEKRIGLMLFGKGNIGARWLELFAREQKS  
 LSARSGFEFVLGAVVDSRRSLLSY  
 DGLDASRTLAFYNDEAKEQDEESLFLWMRAHPFD  
 DLVVLDVTASPSLAEQYLDFASYG  
 FHVISANKLAGASSNNYRQIRDAFAKTGRHWLY  
 NATVGAGLPVNHTVRDLRDSGDSI  
 LAISGIFSGTLISWLFQFDGSEVFTELVDQAWQ  
 GLTEPDPRVDLSGQDVMRKLVLILA  
 REAGYDIEPNQVRVESLVPAGAESGSDVQDFENG  
 EALNQQMIOIRLEAAKEMGLVLRVY  
 ARFDANGKARVGVEAVRTHPLASLLPCDNVFAI  
 ESRWYRDNPLVIRGFGAGRDVTAG  
 AIQSDLNRLSQQLL"  
 /gene="metF"  
 /locus-tag="y0304"  
 /gene="metF"  
 /locus-tag="y0304"  
 /function="enzyme; central  
 intermediary metabolism: Pool,  
 multipurpose conversions"  
 /note="residues 1 to 294 of 294  
 are 86.39 pct identical to  
 residues 1 to 294 of 296 from E.  
 coli K12 : B3941; residues 1 to  
 294 of 294 are 91.83 pct identical  
 to residues 1 to 294 of 298 from  
 GenPept : >gb|AAC72242.1| (U74302)  
 5,10-methylenetetrahydrofolate  
 reductase [Pectobacterium  
 carotovorum]"  
 /codon-start=1

gene 325700..326584

CDS 325700..326584



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/product="5,10-methylenetetrahydro
folate reductase"
/protein-id="AAM83895.1"
/db-xref="GI:21956983"
/translation="MSFFHANQREALNQLSELQ
GQINVSFEFFPPTSEMEDTLWSS
IDRLSTLKPKFVSVIYGANGSERDRTHSIIKGIK
ERTGLEAAPHLTCIDASPTQLRDI
AIDWNNGIRHIVALRGDLPPNSGKPEMYACDLV
GLLKDVGDFDISVAAYPEIHPEAK
SAQADLINLKRKIDAGANRAITQFFDVESYLRf
RDRCVATGIDVIEVPGILPVSNFK
QLQRFATMTNVRVFNWMTSIFDGLDNDPETERKMV
GASVAMDMVKILSREGVKDFHYT
LNRAELSYAICHTLGVPR"
repeat-region complement(326721..3281 /note="insertion element"
72)
gene complement(326762..3273 /insertion-seq="IS1661"
61) /locus-tag="y0305"
CDS complement(326762..3273 /locus-tag="y0305"
61)
/function="IS and transposon
related functions"
/note="IS1661 OrfB transposase;
residues 1 to 198 of 199 are 54.54
pct identical to residues 41 to
238 of 240 from GenPept :
>emb|CAA63547.1| (X92970) orfB
[Escherichia coli]"
/codon-start=1
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/protein-id="AAM83896.1"
/db-xref="GI:21956984"
/translation="MNQHGLLSLIRKKYRSYRA
DGGRASDNLARNFTSEISGLKWC
TDVTEFRVGAQKLYLSVIQDLFNNEIISWHMSER
AALILTCKTLEKALKVKRKEGLM
LHSDQGWHYRTFPMWRSMLEAGIRQSMRKGNC
DNAMVENFFSHLKAEMYHRRKKYDS
ATVLKRDIIVEYIHYNTERTISLKTGGMSPAERYT
QVEKQ"
gene complement(327602..3282 /locus-tag="y0306"
43)
CDS complement(327602..3282 /locus-tag="y0306"
43)
/function="IS and transposon
related functions"
/note="IS1661 DNA-binding protein;
residues 43 to 211 of 213 are
39.64 pct identical to residues 1
to 167 of 173 from GenPept :
>emb|CAA63546.1| (X92970) orfA
[Escherichia coli]"
/codon-start=1
/transl-table=11
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/protein-id="AAM83897.1"
/db-xref="GI:21956985"
/translation="MNRGNPRSGQAIVRKRGVPR

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GPRFALNPRSWIFLSMIWRFGSMK
HPFSTRLAQVHYLSGKATLRETAQFQSVGKSP
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PEFRLCVVRYMMANRCSAADASAHFNIPNETIIQ
NWMKRYREGGKEALNPSTGTPTMP
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KRKALREEKALREQQKKPE"
/locus-tag="y0307"
/locus-tag="y0307"
/notes="residues 3 to 66 of 71 are
32.30 pct identical to residues
328 to 389 of 550 from GenPept :
>gb|AAB88471.1| (AF242881) agaG
[Agrobacterium tumefaciens]"
/codon-start=1
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/db-xref="GI:21956987"
/translation="MTLSAIRNIADKRGASERA
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/locus-tag="y0308"
/locus-tag="y0308"
/function="enzyme; energy
metabolism, carbon: Fermentation"
/notes="residues 21 to 898 of 898
are 82.10 pct identical to
residues 1 to 883 of 883 from E.
coli K12 : B3956; residues 21 to
898 of 898 are 82.10 pct identical
to residues 1 to 883 of 883 from
GenPept : >dbj|BAB38308.1|
(AP002567) phosphoenolpyruvate
carboxylase [Escherichia coli
O157:H7]"
/codon-start=1
/transl-table=11
/product="phosphoenolpyruvate
carboxylase"
/protein-id="AAM83899.1"
/db-xref="GI:21956988"
/translation="MNIASNPASNTKDKWVRGH
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EALGEHILDRVETIRKLSKSRAGNEASRQELLT
TLQNLNDELPLVARAFSQFLNLT
NTAEQYHISPHGEAASNPEALQFLTRLKDKKL
SDQDMRSVADDLSIELVLTAPTE
ITRRTLIIHKLVEVNTCLSQLDHNLDADYERNKIM
RRLRLQLVAQSWHTDEIRKLRPSPV
DEAKWGFVAVVNSLWEGVPAFLREFNEQLNSLD
YRLPVEAVPIRFTSWMGGRDGNP
NVTAEITRHVLLSRWKATDFLRDIQVLVSELS
MSECTPELRELAGGEEVLEPYRQL
MKNVRTQLTNTQAYLEARLKGERVLPHPDLLVSN
DQLWEPLYACYQSLKACGMEIIAN
GQLLDTLRVRVRCFVPLVRIDVRQESTRHTDAIA
ELTRYLGLGDYESWSESDKQAFV

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RELNSKRPLVPLKWEPSAETQEVLETCRVIAEAP
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IDWYRGLIQGKQVMVIGYSDSAKD
AGVMAASWAQYRAQDALIKTCEKAGITLTLFHGR
GGSIGRGGAPAHAAALLSQPPGSLK
GGLRVTEQGEMIRFKFLGPEVTISSLALYAGAIL
EANLLPPEPKKEWIEVMDLLSDA
SCDMYRSYVRENPEFVRYFRAATPELELGLPLG
SRPAKRPPDGGVESLRAIPWIFAW
TQNRMLPWLWAGAGLQRAIDAGKQDVLATMCR
DWPFSTTRIGMLEMVFADLWLA
EYYDQRLVDKSLWPLGQQLRDQLAADIKVVLAIA
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AAGMRNTG"
gene      complement(331869..3330
38)      /gene="argE"
          /locus-tag="y0309"
CDS      complement(331869..3330
38)      /gene="argE"
          /locus-tag="y0309"
          /function="enzyme; amino acid
          biosynthesis: Arginine"
          /note="residues 1 to 386 of 389
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          residues 1 to 381 of 383 from E.
          coli K12 : B3957"
          /codon-start=1
          /transl-table=11
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          deacetylase"
          /protein-id="AAM83900.1"
          /db-xref="GI:21956989"
          /translation="MKMKLPFFIELYRALIATPS
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          GLLLAGHTDTPVYDEGRWTRDPFT
          LTEHDHKLKYLGTADMKGFFAFILDAVRDIDASK
          LTKPLYILATADEETTMAGARYFA
          ANTQLRPDFAIIGEPSTLQPVRAHKGHISNAIRI
          TGQSGHSSDPARGVNAIDLHMHESI
          TQLMALRTTLQERYHNPAFTIPYPTMNFHINGG
          DAANRICACCELHMDIRPLPGLTL
          SDLNELMTEALEPVSQRWPGRLSIDELHPPIPGY
          ECPDHHMVGVIEKLLGERTAVVN
          YCTEAPFIQQVCPTLVLGPGSINQAHQPDFEIDM
          AFIEPTRELIGQLVDHFCQCK"
gene      333283..334287
          /gene="argC"
          /locus-tag="y0310"
CDS      333283..334287
          /gene="argC"
          /locus-tag="y0310"
          /function="enzyme; amino acid
          biosynthesis: Arginine"
          /note="residues 1 to 334 of 334
          are 78.14 pct identical to
          residues 1 to 334 of 334 from E.
          coli K12 : B3958"
          /codon-start=1
          /transl-table=11
          /product="N-acetyl-gamma-glutamylp
          hosphate reductase"

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		<pre> /protein-id="AAM83901.1" /db-xref="GI:21956990" /translation="MLNTLIVGASGYAGAELTAY LNRHPHNMITGLAVSAQSDAGKGL LSDLHPQLKGILDPLQLPLVDVAQAAKGIDVVFL ATAHEVSHDLAPQFLAAGCCVVF DL SGAFRVRDAAFYSQYYGFEHQHFDWLDKAVYGLA EWQSEDIKQAQLIAVPGCYPTASQ LALKPLVDGQLLNDQAQWPVINAVSGVSGAGRKAS MGNSFCEVSLQPYGLFTHRHQPEI VTHLGPVIFTPHLGNFARGILATITCRLKAGVT AQNIADAYHHAYQNKPLVRLYQOG VPALKAVVGLPFCDIGFSVQGEHLIIVATEDNLL KGAAQAQAVQCMNIRFGFPETQSLL " </pre>
gene	334453..335229	<pre> /gene="argB" /locus-tag="y0311" </pre>
CDS	334453..335229	<pre> /gene="argB" /locus-tag="y0311" /function="enzyme; amino acid biosynthesis: Arginine" /notes="residues 1 to 256 of 258 are 84.76 pct identical to residues 1 to 256 of 258 from E. coli K12 : B3959" /codon-start=1 /transl-table=11 /product="acetylglutamate kinase" /protein-id="AAM83902.1" /db-xref="GI:21956991" /translation="MMNPLVIKLGVLDDSEAL ERLFTALVTYREKHERPLVIMHGG GCLVDELMKRLALPVVKKNGLRVTPADQIDIITG ALAGTANKTLLAWAVKHQINAVGL CLADGNTVTVTLLDAELGHVGHKQPGSAAALVQTL LAAGYMPIISSIGITVEGQLMNVN ADQAATALAATLGADLILLSDVSGILDGKGORIA EMTAQKAEQLIAQGIITDGMVVKV NAALDAARSLGRFPVDIASWRHSEQLPALFNGVPI GTRISV" </pre>
gene	335396..336769	<pre> /gene="argH" /locus-tag="y0312" </pre>
CDS	335396..336769	<pre> /gene="argH" /locus-tag="y0312" /function="enzyme; amino acid biosynthesis: Arginine" /notes="residues 1 to 456 of 457 are 89.03 pct identical to residues 1 to 456 of 457 from E. coli K12 : B3960; residues 1 to 456 of 457 are 90.57 pct identical to residues 1 to 456 of 458 from GenPept : &gt;gb AAL22962.1  (AE008892) argininosuccinate lyase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="argininosuccinate lyase" /protein-id="AAM83903.1" /db-xref="GI:21956992" /translation="MALWGGRRFSQAADQRFRKQFN DSLRFDYRLAEQDIIGSVANSKAL VTVGVLNADEQQQLEQALSVLLEEVQANPHAILA </pre>

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LGCGALAGTAYAIDREQLAGWLGF
ASATRNSLDSVSDRDHVELLSASIGMVHLSRF
AEDLIFFNSGEAAFDVLSDRVTSG
SSLMFPQKKNPDALELIRGKCGRVQGALTGMTMTL
KGLFLAYNKDMQEDKEGLFDALDT
WLDC LHMAALVLDGIQVQRPRCKEAAEQGYANAT
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CDS 337368..339860
/gene="hasR"
/locus-tag="y0313"
/function="transport: transport of
small molecules; cations"
/note="receptor for HasA and heme;
residues 42 to 830 of 830 are
55.62 pct identical to residues
122 to 899 of 899 from GenPept :
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[Serratia marcescens]"
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receptor"
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RGIFNGIGGAGAIGGIATFNTINASDFLAPEKEL
GGHIRAMTGDNGTRFIGSGALALG
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P
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ERTTPPGKRAITSTFAQLNIEYDD
WLRLEGGRLRYDQFRLKGNLWLTSTFLOPYTFEN
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PNPFAAERARTWEAGFNIOQSNLFIEDDHFAAK
VAYFDTRIANYINLELKGAKPKFG
GDSFTDVAIVNNLLKTRFRGLEYSYDAGTFYT
NINYTRMIGVNNVCSPIAWLGGQL
SVKYKYVGKVEQIYAVENEVANNYVTCMNANVLF
GSSAYLPGDRGSLTSGRIFDRRL
DFGTVIRYKNGYQDRSAQDENGNNPLTAYVADWPK
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/gene="hasA"
/locus-tag="y0314"
gene 340082..340699

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CDS

340082..340699

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/gene="hasA"
/locus-tag="y0314"
/function="transport: transport of
small molecules; cations"
/note="secreted heme-binding
protein experimentally shown to
bind heme; residues 1 to 181 of
205 are 31.60 pct identical to
residues 1 to 182 of 188 from
GenPept : >emb|CAA57068.1|
(X81195) hasA [Serratia
marcescens]"
/codon-start=1
/transl-table=11
/product="secreted hemophore"
/protein-id="AAM83905.1"
/db-xref="GI:21956995"
/translation="MSTTIQYNSNYADYSSYL
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GSSTLFSGTQYIAIGSSHSNPEGMIAEGDLKYSEF
PQHTFHGQIDTLQFGKDLATNAGG
PSAGKHLEKIDITFNELDLSEGFDSGKSMTEHQQ
GDMHKSVRGLMKGNPDPMLEVMKA
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VVDCHDMLLAA"

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gene 340850..342673

CDS 340850..342673

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/locus-tag="y0315"
/function="transport: transport of
small molecules; cations"
/note="secretion of HasA; residues
22 to 589 of 607 are 62.14 pct
identical to residues 1 to 566 of
582 from GenPept :
>dbj|BAA12015.1| (D83582)
metalloprotease transporter
[Serratia marcescens]"
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secretion system"
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/db-xref="GI:21956996"
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VFVEIGLLEWVRSADVIRLGTQID
MQLNQPVFNAAFAANLKGHNTPAAQALNDLTVLR
QFATGNALFAFFDAPWFPLYLVLI
FLLHPWLGLAAAGAGILVVLAWNQWICKPLH
DASIIITSHATQOANANLRNADVIE
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AVAKSSRQALQSMMLGLGALLVIY
NEITAGVMIAGSILIGRVLGPIDQLIAVWQWNSH
ARLAYQRLSQLLAQHPSSPTGMVL
PAPQGLNVTQLMACKPGTHIPVLHSINFELQPG
DVLGILGPSGSGKSTLAKLLVASQ
PTFSGTVRLDSADLSRWDTQLGEGIFGYLPQNIQ
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gene	342749..344077	
CDS	342749..344077	
		/gene="hasB" /locus-tag="y0317" /gene="hasB" /locus-tag="y0317" /function="transport: transport of small molecules; cations" /note="possibly specific for heme-HasA uptake via HasR receptor; residues 14 to 265 of 267 are 36.90 pct identical to residues 16 to 257 of 258 from GenPept : >gb AAK67308.1  (AF283294) CjrB [Shigella flexnerii]" /codon-start=1 /transl-table=11 /product="TonB-like protein" /protein-id="AAM83908.1" /db-xref="GI:21956998" /translation="MNRLQSSDKLIFWLVGALL ACGIHIYALWWLSTASIPAITSY PAAIMMELSAEPEFMQNLPNQSVVGITQNIIEPA VEQVRNQPDVIDLPTLPEQPEGO 
gene	344142..344945	
CDS	344142..344945	

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REITRKEPIKVKRPAENRATSRKPVNKETQESDS
KQSSPAAAAASAMLSGTSQQVAAAV
NSDSSHRQQAQVSWKSRLLQGHLMGFKRYPSSARK
QQQQTAMIRFVVDKNGYVSSVQL
SHSSGTSALDREALAIKRAQPLPKPPAELLSQG
QITLSLPVDFNLKRRK"
gene      complement(345061..3465 /locus-tag="y0318"
24)
CDS       complement(345061..3465 /locus-tag="y0318"
24)
        /function="enzyme; oxidoreductase"
        /note="residues 1 to 486 of 487
        are 75.00 pct identical to
        residues 1 to 483 of 484 from
        GenPept : >gb|AAF95779.1|
        (AE004330) pyridine
        nucleotide-disulfide
        oxidoreductase, class I [Vibrio
        cholerae]"
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        /transl-table=11
        /product="putative pyridine
        nucleotide-disulphide
        oxidoreductase"
        /protein-id="AAM83909.1"
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        SVETIPAAADKIQGYARFIDNTLQVDDHTQLTSG
        KIIAQRIVIATGSRPSPWASWNEI
        GDRLLIINDVFNWDDLPESSAVFPGVIGLELQG
        ALHRLGVQVKMFGVGGAVGLTDS
        IVRDYAAKITLGDEFYLDPDVKVELMQREGDKVFI
        RYLDKSGRPQEIIMVDYVLAATGRR
        PNVDKLGLENTSLILDERGVFPQADRLTMQTNVPH
        IFIAGDASNQLPLLHEASDQARIA
        GVNAGGFPEVVVPLRRSPISVVFSDPQIAMVGAT
        FRELAQKFSACGCFEIGEVSFENQ
        GRSRVMLKNKGILRIYGEQGTGRFLGAEMMGPSA
        EHIHLLANAHQQQMTIDQMLDMP
        FYHPVIEEGLRTLALRDLQSKLKLGADEAERCLRC
        PGE"
gene      complement(346619..3473 /locus-tag="y0319"
50)
CDS       complement(346619..3473 /locus-tag="y0319"
50)
        /function="enzyme; oxidoreductase"
        /note="residues 1 to 241 of 243
        are 81.32 pct identical to
        residues 5 to 245 of 247 from
        GenPept : >gb|AAF95778.1|
        (AE004330) peroxiredoxin family
        protein/glutaredoxin [Vibrio
        cholerae]"
        /codon-start=1
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        /protein-id="AAM83910.1"
        /db-xref="GI:21957000"

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gene	347497..348414	/gene="oxyR"
		/locus-tag="y0320"
CDS	347497..348414	/gene="oxyR"
		/locus-tag="y0320"
		/function="regulator; global regulatory functions"
		/note="residues 1 to 305 of 305 are 86.55 pct identical to residues 1 to 305 of 305 from E. coli K12 : B3961; residues 1 to 297 of 305 are 91.24 pct identical to residues 1 to 297 of 302 from GenPept : >gb AAC72241.1  (U74302) oxidative stress transcriptional regulator [Pectobacterium carotovorum]"
		/codon-start=1
		/transl-table=11
		/product="activator, hydrogen peroxide-inducible genes"
		/protein-id="AAM83911.1"
		/db-xref="GI:21957001"
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gene	complement(348397..349731)	/gene="udhA"
		/locus-tag="y0321"
CDS	complement(348397..349731)	/gene="udhA"
		/locus-tag="y0321"
		/note="residues 1 to 444 of 444 are 84.00 pct identical to residues 1 to 444 of 444 from E. coli K12 : B3962; residues 1 to 444 of 444 are 85.36 pct identical to residues 23 to 466 of 466 from GenPept : >gb AAL22964.1  (AE008893) soluble pyridine nucleotide transhydrogenase [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative oxidoreductase"
		/protein-id="AAM83912.1"

gene	350003..350650	/db-xref="GI:21957002"
CDS	350003..350650	/translation="MGLVKQGARVAVIERYNNVG GGCTHWGTIPSKALRHAVSRIIEF NQNPYSDNARTIKSSFADILNHADRVINQQTRM RQGFYDRNHCHMFSGDASFIDANT VNVRYADGTSDTLQADNVIATGSRPYPVNVDF NHERIYDSDTILQLSHEFQHVIIY GAGVIGCEYASIFRGLSVKVDLINTRDLLAFLD QEMSDALSYHFWNNGVIRHNEEF EQIEGTTDGVIVHLKSGKKVKADCLLYANGRTGN TSLGLENIGLEADSRGLLKVNNSM YQTALSHVYAVGDVIGYPSLASAAAYDQGRIAAQA MIKGEANVHLIEDIPTGIYTIPEI SSVGKTEQELTAMKVPYEVGRAQFKHLARAQIVG MDTGSLKILFHRETQKILGHCFG ERAAEIIHIGQAIMEQKGEGNTLEYFVNTTFNYP TMAEAYRVAALNGLNRLF" /locus-tag="y0322" /locus-tag="y0322" /note="residues 4 to 210 of 215 are 95.65 pct identical to residues 19 to 225 of 234 from E. coli K12 : B3963" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83913.1" /db-xref="GI:21957004" /translation="MGTIMGVRAQQKERTRRSLI EAAFSQLSAERSFASLSLREVSRE AGIAPTSFYRHFSDVDELGLTMVDESGLMLRQLM RQARQRIAKGGSVIRTSVSTFMEF IGNNPNAFRLLLRERSGTSAAFAAVAREIQHFI AELADYLELENHMPRSFTEAQAEA MVTIVFSAGAEVLDVDIEQRRQLEERLVLQLRMI SKGAYYWRREOEKLAASRVE" /locus-tag="y0323" /locus-tag="y0323" /note="residues 3 to 115 of 135 are 66.37 pct identical to residues 2 to 114 of 119 from E. coli K12 : B3964; residues 3 to 115 of 135 are 70.79 pct identical to residues 2 to 114 of 119 from GenPept : >gb AAL22966.1  (AE008893) putative inner membrane protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83914.1" /db-xref="GI:21957005" /translation="MEQSSRRETGTLALLALITGL AINGVCAALFSALVFFSVFPLLT ILAVYCLHQRYLNFPMQGPVPLASACFLLGILL YSAIVRVEYPAIGSNFVPAVLSVV LVFWILFKLRTKRSVQTHTDADIDINNSDQPPQ"
gene	complement(351204..352307)	/gene="trmA"
CDS	complement(351204..352307)	/locus-tag="y0324" /gene="trmA"

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/locus-tag="y0324"
/function="enzyme; aminoacyl tRNA
synthetases, tRNA modification"
/note="residues 1 to 363 of 367
are 77.41 pct identical to
residues 1 to 363 of 366 from E.
coli K12 : B3965; residues 1 to
363 of 367 are 77.41 pct identical
to residues 1 to 363 of 366 from
GenPept :
>gb|AAG59169.1|AE005628-5
(AE005628) tRNA
(uracil-5-)-methyltransferase
[Escherichia coli O157:H7 EDL933]"
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(uracil-5-)-methyltransferase"
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LELRDQLRAQGGFDLQLIGRAAKTK
IMLDHYDIDEVLFPVAGREMIYRQVENSFTQPNAA
VNIHMLEWALDVTQGATGDLLLEY
CGNGNFSALARNFERVLATEIAKPSVAAAQYNI
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gene 352703..354664
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/locus-tag="y0325"
/function="membrane; outer
membrane constituents"
/note="residues 31 to 653 of 653
are 64.84 pct identical to
residues 2 to 614 of 614 from E.
coli K12 : B3966"
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/product="outer membrane receptor
for transport of vitamin B12, E
colicins, and bacteriophage BF23"
/protein-id="AAM83916.1"
/db-xref="GI:21957007"
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PGVDIAQDGGMGQRSSSLFIRGTNSSHVLVLIDGV
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VTLAGNYTYSKGYDVVAGMPGAGGPRQPDRDGM
GKMLWAGLEHQFNEQFNGFARVYG
FDNRSDYDGYTNYSNPLALIDTRKLSSTRTYDTGL

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		RYKNGIYASQFIASYNRTKDYNS PLFGQHDITASLDEAEQYNLQWNTFQLTNGMIS AGADWQEQRTERKSSNQNTTADFT QHNTGIYLTGQQQISDVTLLEGAVRSDDNSQFGWH STWQTSAGWEFIDGYRLIGSYGTA YKANPLMQLYSAYGGNANLKPEKQWEGGVEGL TGPLTWRLSAYRNDIDQLIDYSNL TNGYFNINKATIKGVEWTSGFDGPLSHQVLEY LDPNRADTHEILVRRAKQQVKYQL DWQVADLDWSTYQYLGQRYDKDYSTEETVEL GGVSLWDLAVSYPTVSHLTVRGRI ANLFDKDYEMVYGQYTPGREYYFTGSYNF" /gene="murI" /locus-tag="y0326" /gene="murI" /locus-tag="y0326" /function="enzyme; murein sacculus, peptidoglycan" /note="required for biosynthesis of D-glutamate and peptidoglycan; residues 9 to 299 of 299 are 71.13 pct identical to residues 1 to 287 of 289 from E. coli K12 : B3967; residues 13 to 299 of 299 are 73.17 pct identical to residues 1 to 283 of 283 from GenPept : >gb AAL22969.1  (AE008893) glutamate racemase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="glutamate racemase" /protein-id="AAM83917.1" /db-xref="GI:21957008" /translation="MPTCLIKIMRWFMATKPQDA NTTSREAITSKADSPRPRTALIFD SGVGGLSVYQEI RQLLPDLHYIYAFDNVAFPYGE KSGE FIVERVLEIVTAVQQRHPLA IVVIACNTASTVSLPALRERFAFPVVGVPVPAIKP AVRLTRNGVVGLLATRATVHASYT LDLIARFATDCKIELLGSSSELVEAETKLHGGVV PLEV LKKILHPWLSMREPPDTIVL GCTHFP LLTEELAQVLP EGT R MVD SGAAIARRTA WLISSQENVISSQDENIAYCMALD EDTDALLPVLQSYGF PKLQKLPI" /locus-tag="yr005" /locus-tag="yr005" /product="16S ribosomal RNA" /locus-tag="yt003" /locus-tag="yt003" /product="tRNA-Glu" /note="anticodon: TTC" /locus-tag="yr006" /locus-tag="yr006" /product="23S ribosomal RNA" /locus-tag="y0327" /note="residues 5 to 36 of 130 are 50.00 pct identical to residues 11 to 48 of 50 from GenPept :
gene	354573..355472	
CDS	354573..355472	
gene	355930..357514	
rRNA	355930..357514	
gene	357608..357680	
tRNA	357608..357680	
gene	357936..360842	
rRNA	357936..360842	
gene	complement(360878..361270)	
CDS	complement(360878..361270)	

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>emb|CAB67146.1| (AJ271079)
hypothetical protein [Oenothera
elata subsp. hookeri]"
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/product="hypothetical"
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/locus-tag="yr007"
/locus-tag="yr007"
/product="5S ribosomal RNA"
/locus-tag="yt004"
/locus-tag="yt004"
/product="tRNA-Asp"
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/note="anticodon: CCA"
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/locus-tag="y0328"
/function="putative regulator"
/note="residues 1 to 318 of 318
are 75.78 pct identical to
residues 1 to 318 of 318 from E.
coli K12 : B4227"
/codon-start=1
/transl-table=11
/product="solute-binding
periplasmic protein of ABC
transporter"
/protein-id="AAM83919.1"
/db-xref="GI:21957011"
/translation="MYRRLLLAAAVTAAMCSAVQ
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GVDAIFIAFPVVGATGTPVLQEAKE
AKIPVFLLDRIEIVNDPSLYTAAVSDSVYEGKV
AGEWLLQDVAGKPCNVVVELQGTVG
SSVAIRNKKKGADGIASAPGVKIIRSQSGDFTRS
KGKEVMESFIKAEQNGKNICAVYA
HNDDMAIGAIQAIKEAGLKPQSDIKIVSIDGVDP
IFKAMSSGEANATVELTPNMAGPA
LDALIVLKKDGTQPPKFIQTESRLLQPDATKQEY
ELKKS LGY"
/locus-tag="y0329"
/locus-tag="y0329"
/function="putative transport"
/note="residues 4 to 376 of 496
are 62.73 pct identical to
residues 9 to 381 of 417 from E.
coli K12 : B4228; residues 4 to
494 of 496 are 67.20 pct identical
to residues 9 to 499 of 500 from
GenPept :
>gb|AAG59426.1|AE005655-5
(AE005655) putative ATP-binding

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gene	360950..361069
rRNA	360950..361069
gene	361193..361272
tRNA	361193..361272
gene	361278..361350
tRNA	361278..361350
gene	362330..363286
CDS	362330..363286
gene	363372..364862
CDS	363372..364862

gene	364874..365893	component of ABC transporter [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ATP transport system" /protein-id="AAM83920.1" /db-xref="GI:21957012" /translation="MEILLEVRGLSVEFPVKAL DSVDFSLQRGEVVALLGENGAGKS TLIKALTGVYKRSAGEVLLDGKAVCPIDTADAQL MGIGTVYQEVNLLPNISVAANLFI GREPLRWGLIDHNKMNQQAAKLLTG YGLTLDVQQ PLANFSIAIQQIVAIARAVDLSAK VLILDEPTASLDAKEVSMLLDILCQLRDQGIGMV FVTHFLDQVYRISDRITVLRNGKL VGTKTVAELFRIELVQMLGHSPFDEQLLKRGEHS ITNKNFLVEFKNYGRRGVVENFDL SVSPGEIVGLAGLLGSGRTEAQLIFGITTPTDG EAKIQGKPKVIRTPRKASKFGEFGY CPEDRKTEGIVGAATVRENIILALQAQRGWLRL SMREQTQIADDFIQQLGIRTPSFE QQIQYLSGGNQKQVLLARWLATKPRFLILDEPTR GIDVGAHAETIRLIEKLCEGLAL LIISSELEELAGYADRIIVLRDRRHVAQLDHDEI SVPAINQAIAYV"
CDS	364874..365893	/locus-tag="y0330" /locus-tag="y0330" /function="putative transport" /note="residues 4 to 326 of 339 are 70.67 pct identical to residues 4 to 325 of 341 from E. coli K12 : B4230; residues 4 to 326 of 339 are 70.37 pct identical to residues 4 to 325 of 341 from GenPept : >gb AAG59427.1 AE005655-6 (AE005655) putative transport system permease protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative ABC transport system inner membrane permease protein" /protein-id="AAM83921.1" /db-xref="GI:21957013" /translation="MGNRSLSMTQRPRKVKWVLP KGATQFGALAVILLIDSLVAPHFF SIHIQDGRLFSGSIIDILNRGAPVALLAGMTLVI ATGGIDLSVGAVMAIAGATAATLT SAGYPFMTVLALS LAVGALCGLWNGFLVAVLQIQ FIVATLMLMVAGRGIAQLITEGQI VTFDSGGLATLGSSSTLMYLPMSVV IACSM LILVW LLTRKTALGLFIESVGINLRSARN AGVSTRVLVIAVYVIGCVGAACAAIIVTADIRGA DANNAGLWLELDAILAVVIGGASL MGGRFNLLLSVIGALIIQGMNTGILLSGYQPEFN LVLKAIIVLAVLVVQSPMISLSHL FQRRK"
gene	365893..366885	/locus-tag="y0331" /locus-tag="y0331" /function="putative transport"
CDS	365893..366885	

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/note="residues 9 to 330 of 330
are 70.18 pct identical to
residues 1 to 318 of 323 from E.
coli K12 : B4231"
/codon-start=1
/transl-table=11
/product="putative ABC transporter
permease protein"
/protein-id="AAM83922.1"
/db-xref="GI:21957014"
/translation="MLKRNVPLLITIAVFILGYA
FCLSQFPFSFSSSRVWCDDLTDNAF
LGIYVAVGMTFVILSGGIDLSVGSVIAFTGVLLAK
LIGTYGIHPVYAFAIVLVMGAMFG
ALMGWIIDSLKLPFAIITLAGMFFIRGMSFIVSE
ESLPINHPYIETLANYAWRVPGGG
RFTLLAFIMLMVAVFGILLAHHTRFGHNVAIGG
NSVSAGLMGVFVRRITIKIYMLSS
TLAALSGIVFSLYTSAGYALAASGVELDAIAAVV
IGGTLLAGGIGTIVFGTLFGVLVIQG
LIQSYITFDGTLSSWWTIKIVIGILLFSFIVIQKA
MSAFYLNRRSRPQSSPLTPV"
gene      complement(366872..3677 /locus-tag="y0332"
53)
CDS       complement(366872..3677 /locus-tag="y0332"
53)

/note="residues 84 to 280 of 293
are 50.99 pct identical to
residues 3 to 190 of 198 from E.
coli K12 : B3762; residues 1 to
281 of 293 are 62.32 pct identical
to residues 1 to 272 of 278 from
GenPept : >emb|CAD09467.1|
(AL627279) possible LysR-family
transcriptional regulatory protein
[Salmonella enterica subsp.
enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83923.1"
/db-xref="GI:21957015"
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YLTPLWQLLYEQQEELRLAARLNSLVKQLHE
RQLDLLITTEPPKMDLACLLGH
FSLRLYSSFSLDLPKEDDTNEHKNASEVPYIKL
EWGADFHQQENRLDSEQAPILTT
TSAHLTRQLLETGGCAFLPEHWOKEYPQLVIHP
DIPPIVRPLYAVNLQNSDQQALIR
QLLKTIPMNNATQSVTRE"
gene      367788..368210
CDS       367788..368210
/locus-tag="y0333"
/locus-tag="y0333"
/note="residues 29 to 140 of 140
are 83.03 pct identical to
residues 1 to 112 of 112 from E.
coli K12 : B3764"
/codon-start=1
/transl-table=11
/product="hypothetical protein"

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/translation="MFCFTRCQAYLILRAINSTT
MRELGAQCQADSFITINRFFDNKH
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EPVTEEEQRFVAVCRGEREPVSAE
EKVWSKYVIRTRQPKRFHTLGGGKQMDAVEDYT
DSDD"
gene      complement(368467..3700 /locus-tag="y0334"
11)
CDS       complement(368467..3700 /locus-tag="y0334"
11)

/function="putative regulator"
/notes="residues 1 to 513 of 514
are 62.76 pct identical to
residues 4 to 515 of 516 from E.
coli K12 : B3765"
/codon-start=1
/transl-table=11
/product="putative 2-component
regulator"
/protein-id="AAM83925.1"
/db-xref="GI:21957017"
/translation="MTAKESIMSLATIHTRATLG
IQAPPVAVEVHISNGLPLGLILVGL
PETIVKEARDRVRSALINSGFNPAKRITVSLAP
ADLPKEGGRYDLPIALAILAASEQ
IPADKLAHYEFLGELALSGALRRVSGAIPAALTC
SEANRQLILPTANGLEIGLIPQGN
SWVADHLLAVCGFLQGENPLAQGQPFEPAPSPDN
HLDLHDIIGQSQAKRALEIAAAGG
HNLLLLGPPGTGKTMALTRLTGLLPFLTDQEALE
AAAITGLLHNSNALPTQWRACRAFFRA
PHHSASMAALIGGGSIPRPGEISLAHNGVFLDE
LPEFERRVLDLSLREPLESGETIIIS
RAAAKICFPAKVQLIAAMNPSPSGHYQGVHNRTF
PQQILRYLAKLSGPFLLDRFDLSIE
VPLLPAAGMLGAQKNQGESSATVKQVRLQARQRM
DRAGKINTQLTSQEVAEFCYLAPE
DAAFLEQVLLTLGLSVRAWHHILKVARTIADLAQ
EKTIQKSHLSEALSYRCMDRLLLQ LHKSLM"
gene      370374..370472
/locus-tag="y0335"
CDS       370374..370472
/locus-tag="y0335"
/function="leader; amino acid
biosynthesis: Isoleucine, Valine"
/notes="residues 1 to 32 of 32 are
81.25 pct identical to residues 1
to 32 of 32 from E. coli K12 :
B3766"
/codon-start=1
/transl-table=11
/product="ilvGEDA operon leader
peptide"
/protein-id="AAM83926.1"
/db-xref="GI:21957018"
/translation="MKAILQVINLVLSVVVVI
PCCGAALGRRKA"
gene      370613..372259
/locus-tag="y0336"
CDS       370613..372259
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/locus-tag="y0336"
/function="enzyme; amino acid
biosynthesis"
/note="residues 1 to 548 of 548
are 79.92 pct identical to
residues 1 to 548 of 548 from
GenPept :
>gb|AAG58963.1|AE005608-4
(AE005608) acetohydroxy acid
synthase II [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
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synthase II"
/protein-id="AAM83927.1"
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LIGTDAFQEIDVGLSLACTKHSFLVESLDALPE
IMAEAFAIATSGRPGPVLIDIPKD
IQLAVGELTPhLKPVEEHSDSAELQHAWDMLA
NAQKPMLYVGGGVGMAQAVPALRD
FIAMTGIPAVATILKGLGAPDIAHPCYLGMLGMHG
TKAANFAVQDCDLLVAVGARFDDR
VTGKLNITFASKAKVIHMDIDPAELGKLRQVHVAL
QGNLNLVLLPALQQPLNIQSWRDEV
MALKQQQHWWRYDHPGQAIYAPLLKQISERKAPE
TVVTITDVGGHQHMTAQHMNFTRPE
NFITSSGLGTMGFGVPAAVGAQMARFPDDMVICVS
GDGGSFMMNVQELGTIKRKLPLKI
VLLDNQRLGMVRQWQQLFFDGRYSETNLSNDPFD
ITLASAFDIPGQRITRKDQVDAAL
DALFNSEGPYLLQVSIIDENNVWPLVPPGAGNET
MLEKIS"
/gene="ilvE"
/locus-tag="y0337"
/gene="ilvE"
/locus-tag="y0337"
/function="enzyme; amino acid
biosynthesis: Isoleucine, Valine"
/note="residues 27 to 332 of 333
are 91.17 pct identical to
residues 3 to 308 of 309 from E.
coli K12 : B3770; residues 27 to
332 of 333 are 91.50 pct identical
to residues 3 to 308 of 309 from
GenPept :
>gb|AAG58965.1|AE005608-6
(AE005608) branched-chain
amino-acid aminotransferase
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="branched-chain
amino-acid aminotransferase"
/protein-id="AAM83928.1"
/db-xref="GI:21957021"
/translation="MSPVSRSYNLIHYRYAPDAP
EGKKRMTKKADYIWFNGEMVPWAE

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gene 372461..373462

CDS 372461..373462

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gene	373725..375623	
CDS	373725..375623	
		375629..377173 /gene="ilvA" /locus-tag="y0339" /gene="ilvA" /locus-tag="y0339" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 1 to 514 of 514 are 84.63 pct identical to residues 1 to 514 of 514 from E. coli K12 : B3772; residues 1 to 514 of 514 are 85.01 pct identical to residues 1 to 514 of 514 from GenPept : >dbj BAB38129.1  (AP002566) threonine deaminase
gene	375629..377173	
CDS	375629..377173	

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[Escherichia coli O157:H7]"
/codon-start=1
/transl-table=11
/product="threonine deaminase
(dehydratase)"
/protein-id="AAM83930.1"
/db-xref="GI:21957023"
/translation="MAVSQPLSAAPCGAEYLRAI
LRAPVYEVAQVTP LQVMKEISSRV
GNTVLVKREDRQPVHSFKLRGAYAMISLTEEQK
ACGVVTASAGNHAQGVALS AHKMG
IKALIVMPVATADIKVDVAFAGGEVLLFGANFD
EAKTKAIALAQEQGYTFVPPFDHP
AVIAGQGT LAMELLQQDAHLDRVFVPVGGGGLVA
GVAVLIKQLMPQIKVIGVEAEDSA
CLRAALDAGQVPDLARVGLFAEGVAVKRIGDEPF
RLCQEYLLDDVITVDS DAICAAVKD
LFEDVRAIAEPSGALAGLKKYVQQHNIQGERL
AHVLSGANVNFHGLRYVSERCELG
EQREALLAVTIPEQKGSFLRFCELLGGRSVITEFN
YRYADAENACIFVGVRLTRGYAER
VEILAE LQDKGYQVVDLSDDEMAKLHVRYMVGGR
PSKPLRERLFSFEFFESPGALLKF
LHTLGTHWNISLFHYRSHGTDGFRVLA AFELSAT
EPQFEERLAALGYCHDET DNPAP KFFLAG"
gene      complement(377304..3777 /locus-tag="y0340"
89)
CDS        complement(377304..3777 /locus-tag="y0340"
89)

/notes="residues 7 to 161 of 161
are 33.72 pct identical to
residues 6 to 167 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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/db-xref="GI:21957024"
/translation="MRLPGAVMKAKSKKIICALL
LLGSILLGYFFWL SRHPVEIISVH
QRNNYS DILVRNFPFTEKGKINWLENRDMLKAK
YSIPKASDGFYTIIFWDFGDGYK
EEGKYDRLCFSDMNTTKNCIEKEKYMTIYKIKND
EPLFSFDGNRYFLNENNKIVMKMR E"
gene      complement(377848..3783 /locus-tag="y0341"
30)
CDS        complement(377848..3783 /locus-tag="y0341"
30)

/notes="residues 7 to 153 of 160
are 37.01 pct identical to
residues 6 to 152 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
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LLGSILLGYFFWLSLRPVEIVAIH
KDGNSFAVLVRDFPVTDKGKINWWLENKSRLKDK
YNIPNPAPDGGFFSITIWDGDKYK
EEGKYDRRCFEDMKTSKNCIDKNSLMIIRNSQYN
VMSFTLDSGIYQLKNGEIVKMKRE "
gene      complement(378389..3788 /locus-tag="y0342"
50)
CDS       complement(378389..3788 /locus-tag="y0342"
50)

/notes="residues 5 to 146 of 153
are 39.35 pct identical to
residues 8 to 152 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhij]"
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/db-xref="GI:21957026"
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GYFFWLSLRPVEIVAVHKDRNFSA
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PDGFFSITIWDGDKYKKEEGKYDR
RCFEDMKTSKNCIDKNSLMIIRNSQYNVMSFTLD
SGIYQLKNGEIVKMKHE"
gene      complement(378834..3797 /locus-tag="y0343"
89)

/notes="disrupted by frameshift"
/pseudo
gene      complement(380665..3815 /gene="ilvY"
49)
/locus-tag="y0344"
CDS       complement(380665..3815 /gene="ilvY"
49)

/locus-tag="y0344"
/function="regulator; amino acid
biosynthesis: Isoleucine, Valine"
/notes="residues 2 to 294 of 294
are 73.72 pct identical to
residues 1 to 293 of 297 from E.
coli K12 : B3773; residues 2 to
294 of 294 are 74.06 pct identical
to residues 1 to 293 of 297 from
GenPept :
>gb|AAG58968.1|AE005608-9
(AE005608) positive regulator for
ilvC [Escherichia coli O157:H7
EDL933]"
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/transl-table=11
/product="positive regulator for
ilvC"
/protein-id="AAM83934.1"
/db-xref="GI:21957027"
/translation="MMDLRDLKVFLHLAESRHF
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LLHALGQHGPSLSGELRLFCSVTA

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gene	381832..383310	AYSHLPPIILDRFRARHPVLVEIKLTTTGDAADAVNM VQSNEADLGIAGRPEVLPTSVAF QIGIEPLVLIAPALPCAVRSQVAVEKPDWAMIPF ILPEHGPSRRKRIIDLWFRRQRIITNP LIYATVSGHEAIVSMVALGCGVALIPSVVVDNSP EPVRNRISLLDDVSLVEPEFELGVC VPKKRLQEPIDAFWGLL" /gene="ilvC" /locus-tag="y0345" /gene="ilvC" /locus-tag="y0345" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 1 to 492 of 492 are 92.07 pct identical to residues 1 to 491 of 491 from E. coli K12 : B3774; residues 1 to 492 of 492 are 92.27 pct identical to residues 1 to 491 of 491 from GenPept : >emb CAD09408.1  (AL627279) ketol-acid reductoisomerase [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="ketol-acid reductoisomerase" /protein-id="AAM83935.1" /db-xref="GI:21957028" /translation="MANYFNTLNLRQQLAQLGKC RFMARDEFADAEAGYLKGKKVIVIG CGAQLNQGLNMRDSDLVAYALRKEAIAEKRAS WRKATENGFKVGTYYEELIPQADLV VNLTDPKQHSAAVKAQVPLMKEGALGSHGFNI VEVGEQVRKIDI TVVMVAPKCPGTE VREEYKRGGFVPTLIAVHPENDPKGEGMAIAKAW AAATGGHRAGVLEFSFVAEVSDDL MGEQTILCGMLQAGSLLCDFKLVSSEGTDAAYAEK LIQFGWETITEALKQGGITLMMDR LSNPAKLRAYALSEQLKEIMAPLFQKHMDDIISG AFSSGMMADWANDDVKLLNWREET GRTAFENAPQFEGKISEQEYFDHGVLMIAMVKAG VELAFETMVDSGIIEESAYYESLH ELPLIANTIAARKRLYEMNVVISDTAEYGNLYFAN AAVPLLKEKFMDSLQAGDGLGKSI GSAVDNAQLRDVNEATRNPHEAVGHKLRGYMTD MKRIAVAG" /locus-tag="y0346" /locus-tag="y0346" /note="residues 15 to 60 of 66 are 34.78 pct identical to residues 525 to 567 of 612 from GenPept : >gb AAL32622.1  (AY062544) Phospholipase like protein [Arabidopsis thaliana]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83936.1" /db-xref="GI:21957030" /translation="MLYYEPEFLGSLROEAYNT
gene	383491..383691	
CDS	383491..383691	

gene	383887..385329	EIAKTEREVAERNRVQKKPFGLFI
CDS	383887..385329	EEMTLQKTLTDSQVAETAHHIT"
		/locus-tag="y0347"
		/locus-tag="y0347"
		/note="residues 340 to 454 of 480
		are 44.16 pct identical to
		residues 257 to 376 of 386 from
		GenPept : >emb CAD16923.1
		(AL646075) probable transmembrane
		protein [Ralstonia solanacearum]"
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		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83937.1"
		/db-xref="GI:21957031"
		/translation="MGLLMQQQRVNADLETAKIT
		EPQRVENARLTAEAAEKAARDRI
		SEEIAATEAKRQRMENERLAEQERQVEGTKQQV
		SEASCAQQASAWQNRFTLPALQFS
		GSAQYSFAASGMSAVGEAAELHNSFLAAQEQLSA
		IATISASGSAAMIALGIYQTKVG
		ESSERPPGWNVSPKFVGSISLSAMGLPATESLAS
		QGMALPVRMRIIDAKDWIGCTEI
		YAVKTGVAGVLPKVKVGAQYDESTGVYTFITDS
		TPPRTLITPAQPPGAETRPILAP
		PGSTPATLQHTGEMIIKPVITPTILPLPQLYARD
		FHDYIIWFPADSGLEPVVYVLSNP
		YGKTTAKGKYSGRDFNPDKAGGPINLWDKEIKI
		RGEVDEVKLHTRRFGELEDNKL
		IERLEKILTNKLTATDIDKRFYTHEIRELERYRM
		LGIPDDVNDKSVWNDAHTATLEDF
		KINEKTQPLYTSEADAYIKAEKLSLGSK"
gene	complement(386990..3878	/locus-tag="y0348"
	08)	
CDS	complement(386990..3878	/locus-tag="y0348"
	08)	
		/function="putative factor;
		folding and ushering proteins:
		Chaperones"
		/note="pili assembly; residues 42
		to 262 of 272 are 46.46 pct
		identical to residues 7 to 227 of
		237 from GenPept :
		>gb AAG05520.1 AE004640-9
		(AE004640) probable pili assembly
		chaperone [Pseudomonas
		aeruginosa]"
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		/transl-table=11
		/product="putative pilus
		chaperone, PapD family"
		/protein-id="AAM83938.1"
		/db-xref="GI:21957032"
		/translation="MHMRKWLVSNNIMLSRINR
		RLRGLLLMTTCRVLTLPALTIGV
		LIMSALATSAVASVIAERTRIVFSEGSTEESLQL
		VNSNSYPVAVQVWVDDGNLMATPD
		KAVSPILVLPPVFRLPQQAQSLRLILSGGSKLP
		ADRESAFWLNLIYEIPPKATPKSGD
		ESFVTALALRMQYKVFYRPNLPAAPGDILGKALT
		SLERNGDSALIKVNNPTPYASFA
		ALTIGSAEGPPMEMVAPFSQLDFFLNRAPISDNKT

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gene      complement(387774..3889 /locus-tag="y0349"
46)
CDS       complement(387774..3889 /locus-tag="y0349"
46)
          /note="residues 2 to 390 of 390
          are 45.88 pct identical to
          residues 56 to 453 of 453 from
          GenPept :
          >gb|AAG05519.1|AE004640-8
          (AE004640) hypothetical protein
          [Pseudomonas aeruginosa]"
          /codon-start=1
          /transl-table=11
          /product="conserved hypothetical
          protein"
          /protein-id="AAM83939.1"
          /db-xref="GI:21957033"
          /translation="MGSRDDNNGSLNLPISIVDLS
          TNANFQPDGTLTASATSDFTTFV
          NTGYALDQVLFRCDAADVQDLYEMYATNGDSTYG
          GRYEDGTIAGNVSYGYATTVMNVV
          IRFTNLATGEYYARIWKRRRLTGLDSTDSSGRILV
          KAKNFSNVYTLEFRIDYARSGANN
          TPSYLYGRSQPNAYIAFKGPGITGPIEGTDSYSN
          WPGWYSTWPAASGLYKYVTFERRIT
          ICAVSNFTPTVVLPRISVAELNNGNTSSADFNVD
          FQCQTGINSQVITAGTVAMGFLVPA
          ANAAKAQALGLMNGNGGVSHLVSDNYGAAGTAGG
          VGIIRYNNSPMYLLSKNVQTGN
          NGGWYIGILQGAQETTSVDGGNSYTETFRALSK
          ISGQTVITAGAVNAHAQVVIRVQ"

gene      complement(389158..3917 /gene="fimD"
85)
CDS       complement(389158..3917 /gene="fimD"
85)
          /locus-tag="y0350"
          /function="membrane; cell
          envelope: outer membrane
          constituents"
          /note="fimbrial biogenesis;
          residues 31 to 874 of 875 are
          46.38 pct identical to residues 25
          to 860 of 872 from GenPept :
          >gb|AAG05518.1|AE004640-7
          (AE004640) probable fimbrial
          biogenesis usher protein
          [Pseudomonas aeruginosa]"
          /codon-start=1
          /transl-table=11
          /product="outer membrane usher
          protein FIMD precursor"
          /protein-id="AAM83940.1"
          /db-xref="GI:21957034"
          /translation="MVQARVILKKNFSGRRKALT
          LCITLILHIDTAFGQEEPQNFEFD
          ESLFLGTKYASGLTQLNKKNSITAGNYDAVDVLV
          NNKLFKRMSVQFIKDANSSEVYPC
          LSEDELLTAAGVELGRENSPPKPEPHVTEANTPIT
          ETHAPTNQCLPLSTRVKGSFRFD
          QAKLRLELSIPQALLQKRPRGYIERAEWQEGEKL

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AFINYSANAYRSDTRGQQKRTSDF  
 GFIGLKSGINLGLWQVRQQSNVRYASNDSGSDTQ  
 WNSIRTYVQRP IPQLDSQLTLGET  
 FTDSTLFGSMSFLGAKMATDQRMWPVSMRGFSPE  
 VRGVASTNARV IIRONGREIYETN  
 VAPGPFVINDLFSTSSQGDLNVEVIEANGSRSTF  
 TVPFSAPVDSMRPGVSRYNAVIGE  
 SRDFTNIDNYFTDFTYERGLINQLTANSQVRLAK  
 DYTALLAGGVLGTFVGALGLNATY  
 SHAKVENDKTQDGRMQATYSQTFNQGTTFSLA  
 GYRYSTKG YRDLNDVFGVRSMQKN  
 GGTWDSSTYKQRSQFTTTINQDLGNWGQLYASAS  
 TSDYYNDTARDTQLQLGYSNSYQQ  
 ISYNLAVSRQRSVYTTLYNWDSPDTDETATTTT  
 YGNTENIATFTVSIPLNIGSNNOY  
 LMSASARNPKSGNNYQTSLSGTAGERNSFNALN  
 AGYDDSNFGSSSNWGANVQKQFP  
 NATVNGSYSRGNNYTQYGAGAGAIVHRQGVTL  
 GPYLGTFGLIEANGAQGARIDSN  
 GFALVPALTPYNYNTIGLDTKGINRNTELKENQG  
 RVVYPAGAAVKVKFETLTGYAVLI  
 QAEGEGPLGADVYNSKDELVMGMVGQGNQIYARI  
 ADNKGTLDVWVGESSGDQCQLPYA  
 FNRQDTEQDIIHITASCRR"

gene complement(391813..3925 /locus-tag="y0351"  
 68)  
 CDS complement(391813..3925 /locus-tag="y0351"  
 68)

/function="putative factor;  
 folding and ushering proteins:  
 Chaperones"  
 /note="pilus assembly; residues 24  
 to 242 of 251 are 43.69 pct  
 identical to residues 16 to 237 of  
 248 from GenPept :  
 >gb|AAG05517.1|AE004640-6  
 (AE004640) probable pili assembly  
 chaperone [Pseudomonas  
 aeruginosa]"  
 /codon-start=1  
 /transl-table=11  
 /product="chaperone"  
 /protein-id="AAM83941.1"  
 /db-xref="GI:21957035"  
 /translation="MTSEGLTILMSIYARHYHYL  
 FVTLLVAMLSLFANASVVMGTGSRI  
 IYPAAASEHSIQLTNNDNFPNAVQVWLDSGDEKS  
 TPETGKAPFIVTPPFRIEANSQO  
 TLRKYTGSGGLPTDRESVFYLNFLQIPPVNKVEK  
 DNKMLVLLRNRIKVFYRPESIIGR  
 VDQVSTALTFLSRKQGTNLVLTGKNPTGFYATIA  
 SGEIVSGIKLKVKSNMIAFMSQV  
 EWVIPNASVSSSATINFLIMNDFGGQDAGSYRI"

gene complement(392608..3931 /locus-tag="y0352"  
 38)  
 CDS complement(392608..3931 /locus-tag="y0352"  
 38)

/function="structural component;  
 cell exterior constituents:  
 surface structures"  
 /note="fimbrial biogenesis;  
 residues 1 to 175 of 176 are 49.15



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pct identical to residues 3 to 177
of 178 from GenPept :
>gb|AAL19294.1| (AE008710)
putative fimbriae; major subunit
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="fimbrial protein
(precursor)"
/protein-id="AAM83942.1"
/db-xref="GI:21957036"
/translation="MKKITLAIALFSASTTVAMS
ASNNTITFQGEVTAQTCSVTVNGL
EANPVVLLPTVSSDDLDA SGQTKGKTTFTLGVSG
CTSGSDDLDIKTVFIGSLVTATGN
LQNTGTAGNVELQLLKDATTTTGIDLNSGLAQDG
IVLLAGDTSAEHDFAVQYYATGQS
TPGSVIASVQYAVSYL"
repeat-region complement(393913..3952
27) /note="insertion element"
/insertion-seq="IS285"
gene complement(393948..3951
56) /locus-tag="y0353"
CDS complement(393948..3951
56) /locus-tag="y0353"
/function="IS and transposon
related functions"
/note="residues 1 to 402 of 402
are 100.00 pct identical to
residues 1 to 402 of 402 from
GenPept : >gb|AAC13227.1|
(AF053947) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
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/db-xref="GI:21957038"
/translation="MDEKKLKALAAELAKGLKTE
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NTPRDRNTFEPQLIKKNQTRITQ
MDSQILSLYAKGMTTREIVATPKEMYDADVSPIL
ISKVTDVAVKEQVAEWQNRQLDALY
PIVYMDICIVVKVRQSGSVINKAVFLALGINTEGQ
KELLGMWLAENEGAKFWLSVLTSL
KNRGLQDILIIACVDGLKGFPDAINSVYPQTHIQL
CIIHMVRNSLKYVSWKDYKAVTSG
LKMVYQAPTEEAALMALDKFAEAWDDKYPQISKS
WRTHWENLNTFFGYPPDIRKAIYT
TNAIESVNSVIRAAIKKRKVFPTDDSVRKVVYLA
IKDASKKWSMPIQNWRLMSRFII
EFGDRLSDHL"
gene complement(395253..3960
44) /locus-tag="y0354"
CDS complement(395253..3960
44) /locus-tag="y0354"
/function="enzyme; global
regulatory functions"
/note="residues 8 to 258 of 263
are 39.45 pct identical to
residues 3 to 256 of 288 from

```

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GenPept : >gb|AAC27745.1|
(AF061240) glutamine
cyclotransferase precursor [Carica
papaya]"
/codon-start=1
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/product="glutamine
cyclotransferase"
/protein-id="AAM83944.1"
/db-xref="GI:21957039"
/translation="MEILNIPRCFTFLIIITY
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DETSFTQGLVIDDGKLYETGLYKNSKIRELDLT
NGKVIRSVNLPDNIFGEGITKLG
SFYVLTWKEKAFVINPNDLKIIFNYEGEGWG
LTTDGINLIMGDSDTLYFRNPAD
FSIIKISVIFDGRRIEKINELEWIDGMIYANVW
YSDAILVIEPENGRRVVKWIELSGL
QFMLDSVNRNTNLTNGIAYDKSKNKIYLTGKNWS
NIFEVKFLTSK"
gene      complement(396283..3965
79)      /gene="ppiC"
CDS      complement(396283..3965
79)      /locus-tag="y0355"
          /gene="ppiC"
          /locus-tag="y0355"
          /function="enzyme; proteins -
translation and modification"
          /note="rotamase C; residues 6 to
98 of 98 are 67.74 pct identical
to residues 1 to 93 of 93 from E.
coli K12 : B3775"
          /codon-start=1
          /transl-table=11
          /product="peptidyl-prolyl
cis-trans isomerase C"
          /protein-id="AAM83945.1"
          /db-xref="GI:21957040"
          /translation="MVTVTMANKASALHILVDDE
KQANDILAQLNNGANFQELAKKFS
NCPSKRNGGDLGEFNKGDMPAFDKAVFSCCELLQ
PYGPVKTQFGYHIKVLIRS"
gene      396714..398789
          /gene="rep"
          /locus-tag="y0356"
CDS      396714..398789
          /gene="rep"
          /locus-tag="y0356"
          /function="enzyme; DNA -
replication, repair,
restriction/modification"
          /note="residues 19 to 686 of 691
are 85.02 pct identical to
residues 1 to 668 of 673 from E.
coli K12 : B3778; residues 19 to
686 of 691 are 85.32 pct identical
to residues 1 to 668 of 673 from
GenPept :
>gb|AAG58972.1|AE005609-4
(AE005609) rep helicase, a
single-stranded DNA dependent
ATPase [Escherichia coli O157:H7
EDL933]"
/codon-start=1

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/transl-table=11
/product="rep helicase, a
single-stranded DNA dependent
ATPase"
/protein-id="AAM83946.1"
/db-xref="GI:21957041"
/translation="MAFWYNSLPRKPIEQPSVMR
LNPSQQEAEVFEVIGPCLVLGAGS
GKTRVITNKIAHLIRQCQYQPKHIAAVTFTNKAA
REMKERVAQTLGRKEARGLMIATF
HTLGLEI IKKEYVALGKMSNFSLFDAQDQMGLLK
DLTHKWLEDDKTLQQLVSAISNW
KNDLLDPAAAAATARSERDKLFVHCYGLYDAHLK
ACNVLDFFDDLISLPTLLQKNLEV
RERWQNRLRYLLVDEYQDNTISQYQMVKLLVGNR
ARFTVVGDDDDQSIYSWRGARFQNL
VLLNEDFPALRVIKLEQNYRSSGRILKAANILIA
NNPHVFEKKLFSLSYGDELKVIT
ANNEDHEAERVVGELIAHHFVKKTQYSDYAILYR
GNHQSRLFELKMLQNRIPYRISGG
DSFFSRPEIKDLLAYLRVLTNQDDSAFLRIVNT
PKREIGAATVQKLGEWANLRNKS
FRASFDLGLGEHLKGRGLESQRFTHWMDGIIRL
VEREPVAAVRDLIHGIDYESWLFE
TAPSPKAAEMRMKNVNLFSWMTEMLGSELDEP
MILTQVVTRFTLRDMMERGESDEE
LDQVQLMTLHASKGLEFFYVFLVGMEEGLPHQS
SIDEDNVDEERRLAYVGITRAQRE
LFFTLCKERRQYGLIRPEPSRFLMELPODDLNW
ENERKAVSPPEERMQKQSHLANLR
AQLANAKKP"

```

```

gene      complement(398790..3989 /locus-tag="y0357"
54)
CDS       complement(398790..3989 /locus-tag="y0357"
54)

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/note="residues 7 to 46 of 54 are
40.00 pct identical to residues
1819 to 1858 of 2565 from GenPept
: >gb|AAL12620.1| (AY051318)
Vitelisin [Penaeus semisulcatus]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83947.1"
/db-xref="GI:21957042"
/translation="MLVGITHSISATLKTSRLMV
NQSRLNAWLTGNRLFPVLIIFTTVA
AFRVNYGFSY"

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gene      complement(398957..4004 /locus-tag="y0358"
52)

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```

/note="gppA; disrupted by
frameshift"
/pseudo
/gene="rhlB"

```

```

gene      complement(400456..4017 /locus-tag="y0359"
42)
CDS       complement(400456..4017 /gene="rhlB"
42)

```

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/locus-tag="y0359"
/note="residues 1 to 428 of 428
are 88.78 pct identical to
residues 1 to 421 of 421 from E.

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		coli K12 : B3780" /codon-start=1 /transl-table=11 /product="putative ATP-dependent RNA helicase" /protein-id="AAM83948.1" /db-xref="GI:21957043" /translation="MSKTHLLEQKFSDFALHPLV VEALENKGQCYCTPIQALALPLTL SGRDVAGQAQTGTGKTLAFLASTFHYLLSHPAEE GRQTNQPRALIMAPTRELAVQIHS DAESLSQVTGLKLGLAYGGDGYDKQKVLESQVD ILIGTTGRLIDYAKQNYINLGAIQ VVVLDEADRMVDLGFIKDIRWLFRRMPSPVDKRLN MLFSATLSYRVRELAFAEQMNAEY VEVEPLQKTGHRIKEELFYPSNEEKMRLQLTIE EEWPDRCIIFANTKHKRCEEIWGHL AADGHRVGLLTGDVAQKKRLRILEDFTKGDLDL VATDVAARGLHPLVTHVFNYDLP DDCEDYVHRIGRTGRAGESGHSISLACEYALNL PAIETYTGHSIPVSKYNSDALLTD LPAPKRLARTRTGNPPRRNSAPRRSGAPRRNNRKR PG" 
gene	401861..402187	/gene="trxA"
CDS	401861..402187	/locus-tag="y0360" /gene="trxA" /locus-tag="y0360" /function="enzyme; biosynthesis of cofactors, carriers: Thioredoxin, glutaredoxin, glutathione" /note="residues 1 to 108 of 108 are 87.03 pct identical to residues 19 to 126 of 127 from E. coli K12 : B3781; residues 1 to 108 of 108 are 87.03 pct identical to residues 1 to 108 of 109 from GenPept : >gb AAC40210.1  (AF044308) Escherichia coli thioredoxin [Cloning vector pBIOTRX-BirA]" /codon-start=1 /transl-table=11 /product="thioredoxin 1" /protein-id="AAM83949.1" /db-xref="GI:21957044" /translation="MSDKIIHLSDDSFDTVLKA SGLVLVDFWAEWCGPCKMIAPILD EIAEYEGRLTIAKLNIDNQGTAFFKYGIRGIPT LLLFRDGEVVATKVGALSKGQLKA FL DANL" 
gene	402667..403926	/gene="rho"
CDS	402667..403926	/locus-tag="y0361" /gene="rho" /locus-tag="y0361" /function="factor; RNA synthesis, modification, DNA transcription" /note="residues 1 to 419 of 419 are 95.22 pct identical to residues 1 to 419 of 419 from E. coli K12 : B3783" /codon-start=1 /transl-table=11 /product="transcription 

gene 404461..405558  
CDS 404461..405558

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termination factor Rho; polarity
suppressor"
/protein-id="AAM83950.1"
/db-xref="GI:21957045"
/translation="MNLTELKNTPVSDLITLIGEN
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SGEDIFGDGVLEILQDGFGLRSADSSSYLAGPDD
IYVSPSQIRRFNLRTGDTVAGKIR
PPKEGERYFALLKVNENYDKPENARNKILFENL
TPLHANSRLRMERGNSTEDLTAR
VLDLAPSIGRGQRLIVAPPKAGKTMLLQNIATS
IAYNHPDCVLMVLLIDERPEEVTE
MQRLVKGEVIASTFDEPASRHOVAEMVIEKAKR
LVEHKKDVIILLDSITRLARAYNT
VVPASGKVLTTGGVDANALHRPKRFFGAARNVEEG
GSLTIIATALVDTGSKMDEVIYEE
FKGTGNMELHLSRKIAEKRVFPAIDFNRSCTRKE
ELLTTTDELQKMWILRLRILHPMGE
IDAMEFLISKLATAKTNDQFFDNMRRS"
/gene="rfe"
/locus-tag="y0362"
/gene="rfe"
/locus-tag="y0362"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/notes="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 357 of 365
are 80.95 pct identical to
residues 1 to 357 of 367 from E.
coli K12 : B3784; residues 1 to
357 of 365 are 81.23 pct identical
to residues 1 to 357 of 367 from
GenPept :
>gb|AAG58979.1|AE005610-3
(AE005610)
UDP-GlcNAc:undecaprenylphosphate
GlcNAc-1-phosphate transferase;
synthesis of enterobacterial
common antigen (ECA) [Escherichia
coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="UDP-GlcNAc:undecaprenylp
hosphate GlcNAc-1-phosphate
transferase"
/protein-id="AAM83951.1"
/db-xref="GI:21957047"
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LFVARKVAIKIGLVDPKNYKRKHQ
GLIPLVGGISVFAGVCF AFLITNQQIPHFRLYLA
CAGLLVFGALDDRFDISVKIRAF
VQALVGIAMMAVAGLYLRS LGHAFGPWEMVLGPF
GYVVTLVFAVAAINAFNMVDGIDG
LLGGLSCVSVFAMGILLYQSGQMSLALWCFAMIA
TIIPYILLNLGLGRRYKVFMGDA
GSTLIGFTAIWILLQATQGNAPHPINVTALWIIA
IPLMDMIAIMYRRLRKGMSPFSPD
RQHIHLIMRAGFTSRQAFVLITLAAALLAMIGV
IGERLTFIPEWMLALFLAFLLY

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gene	405576..406655	GYCIKRAWRVARFIKRFKRRMRASKNKHES" /gene="wzzE" /locus-tag="y0363" /gene="wzzE" /locus-tag="y0363" /function="putative transport" /note="residues 22 to 357 of 359 are 68.15 pct identical to residues 15 to 349 of 349 from E. coli K12 : B3785" /codon-start=1 /transl-table=11 /product="putative transport protein" /protein-id="AAM83952.1" /db-xref="GI:21957048" /translation="MMKPESMSTDKTGSTNNEPS VDNELDIRGLCRTLWRGKVIWIGM AIIFAAIALGVSYLVKQQWSATAITDKPTVNNLG GYYSQQQFLRNLNLRNLSGLVSEQ PGISDEAYGEFITQLAAYDTRRDFWLQSDYYKQR LEGDAKADAALLDELVNNIVFTAR DDKKIPNDSIKLTAETASDANKLLRGYIDFASQR ASSHLNDEIQGAAWARTQSMKAQV KRQEAQAQAVFDREVAVKQALKVAGQQGITSSQ TDTPAEQLADSKMFMLGKPMLEAR LETLLATGSPFDDIDYQNRAMLATLNVGPTLDDK FQTYRYLRTPEDPVTRDSPRRVFL LIMWGAIGALVAGVVLVRRSSKAL" /gene="wecB" /locus-tag="y0364" /gene="wecB" /locus-tag="y0364" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 15 to 394 of 394 are 78.15 pct identical to residues 11 to 389 of 389 from E. coli K12 : B3786; residues 15 to 394 of 394 are 78.42 pct identical to residues 11 to 390 of 390 from GenPept : >gb AAG58981.1 AE005610-5 (AE005610) UDP-N-acetyl glucosamine -2-epimerase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="UDP-N-acetyl glucosamine -2-epimerase" /protein-id="AAM83953.1" /db-xref="GI:21957049" /translation="MRPTCRHCLRLTDLKRFVTK VLTVFGTRPEAIKMAPLVHALAQD DAFESRVCVTAQHREMLDQVLRLEIQPDYDLDI MRPQQLTEITCRILEGLKPVLEE
CDS	405576..406655	
gene	406882..408066	
CDS	406882..408066	

		FKPDVILVHGDTTTTSLASLAGFYHRIPVGHVEA GLRTGDLSPWPPEANRLTGHILA MYHFAPTENSQRNLLREWVPENRIFVTGNTVIDA LFVWRDRVMNTPDLRANLAQRYAF LDTNKKMILVTGHRRESFGGGERICSALAEIAR KHPEVQVVYPVHLNPNVSEPVNRI LKGDINILIDPQDYLFPVYLMNHAYLILTDSSG IQEEAPSLGKPVLMRDTTERPEA VDSGTVLLVGTNINKIVDAVTRLLTDEATAYHQM RAHNYPGDGYACQRILKALNHQV TL"
gene	408063..409325	/gene="wecC"
CDS	408063..409325	/locus-tag="y0365" /gene="wecC" /locus-tag="y0365" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 1 to 420 of 420 are 82.14 pct identical to residues 1 to 420 of 420 from E. coli K12 : B3787; residues 1 to 420 of 420 are 83.57 pct identical to residues 1 to 420 of 420 from GenPept : >emb CAD09395.1  (AL627279) UDP-ManNAc dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="UDP-N-acetyl-D-mannosami nuronic acid dehydrogenase" /protein-id="AAM83954.1" /db-xref="GI:21957050" /translation="MSFETISVIGLGYIGLPTAA AFASRKKKIVIGVDVNAHAVETINR GAIHIVEPDLKVVKIAVEGGYLQAVTKPQAADA FLIAVPTPFKGDPDMIFVESAA KSIAPVLKKGDLVILESTSPVGATEQMAQWLAE RPDLSPFPQAGEAADINIAICYPER VLPQVMVELIQNDRVIGGMTPKCSARASALYKI FLEGECVVINSRTAEMCKLTENSF RDVNIAFANELSLICDEQGINVWELIRLANRHR VNILQPGPGVGGHCIAVDPFVVS QNPQLARLIHTARLVNDGKPLWVVDVRVKAADV LAASDKRASEVKIACFGLAFKPD DDLRESPAVGVARLIAEWHVGETLVVEPNVEQLP KSLMGLVTLKDTATALLQADVLV LVDDHKQFKAIPEDIKQQWIVDTKGVWR"
gene	409316..410389	/gene="rffG"
CDS	409316..410389	/locus-tag="y0366" /gene="rffG" /locus-tag="y0366" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="residues 3 to 355 of 357 are 82.15 pct identical to residues 1 to 353 of 355 from E.

coli K12 : B3788; residues 1 to 357 of 357 are 85.43 pct identical to residues 1 to 357 of 357 from GenPept : >gb|AAC12869.1| (AF044332)  
dUDP-D-glucose-4,6-dehydratase; RffG [Pectobacterium carotovorum subsp. atrosepticum]"  
/codon-start=1  
/transl-table=11  
/product="dUDP-glucose 4,6-dehydratase"  
/protein-id="AAM83955.1"  
/db-xref="GI:21957051"  
/translation="MALRRILVTGGAGFIGSAVV RHIIDGTSDSVVVDKLTYYAGNLE SLSVVAGSERYAFEQVDICDSSSELDRVFAQYQPN VVMHLAAESHVDRSIDGPAAFIET NVVGYTTLLEAARHYWQQLSVEAKQAFRFHHIST DEVYGLDHLGTDLLFTETTPYAPSS PYSASKASSDHLVRAWLRITYGLPTLVNCSNNYG PYHFPKLIPLVILNALAGKPLPV YNGGAQVRDWLYVEDHARALYQVVTGVGETYN IGGHNERKNIEVVETICALLDELV PAKPAGIAHYRDLITYVKDRFGHDMRYAIDAGKI ERELGWRPQETFESGIRKTVLWYL NNESWWRVRVQDGSYAGERLGLSD"  
/gene="rffH"  
/locus-tag="y0367"  
CDS 410474..411565 /gene="rffH"  
/locus-tag="y0367"  
/function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions"  
/notes="residues 71 to 363 of 363 are 86.68 pct identical to residues 1 to 293 of 293 from E. coli K12 : B3789"  
/codon-start=1  
/transl-table=11  
/product="glucose-1-phosphate thymidyltransferase"  
/protein-id="AAM83956.1"  
/db-xref="GI:21957052"  
/translation="MLAAFLHLEIYSVYRWATYE RHQSRLIIGMASSRLHDVLPVYS LCLMVSGDGMVQEIVCIRRLHVSGERMKGILAG GSGSRLHPITRGVSKQLLPYDKP MIYPLSVLMLAGIRDVLIISTPEDLPSPQRLLG NGDEFGINLSYAAQSPDGLAQAF IIGEAFLDNEPCCLVLGDNIYFCQGFSPKLKAVA ARQQGATVFGYQVMDPERFGVVEF DDNFRALSIEEKPSQPKSNWAVTGLYFYDNQVVD FAKQVKPSARGELEITSINQMULD RGLTLVELLGRGFAWLDTGTHDSLIEASTFVQTV EKRRQGFKIACLEEIAWRNGWLDDG GVKRAATALAKTYGKYLLDLLHARPRQY"  
/gene="wecD"  
/locus-tag="y0368"  
gene 411486..412280 /gene="wecD"  
CDS 411486..412280 /locus-tag="y0368"



		/note="residues 63 to 263 of 264 are 49.25 pct identical to residues 1 to 181 of 181 from E. coli K12 : B3790" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83957.1" /db-xref="GI:21957053" /translation="MRQPRWRKPFVMANICWIYYM PVHASIEPLGWSEFFQSQAKLI FSDSAPPLNPAELAAFTLVQAKVPTHRLDLIDAL SQLDFHLVEGEIDLSLVVGEKEGI GTENATSEPNMGAYSLRVATEADIPQLRRVAASA FALSFRFAPWYDAQDSGRFYALWV EKAVLGTDFDHQCLLVLDPTDQPVGFVTLRDLQDG SARIGLLAVFPQAQSKGIGLRRLMS AAKQWCQHHGLHRLRVATQMSNIAALRLYIRSGA SIESTAYWLRCG" /gene="wecE" /locus-tag="y0369" /gene="wecE" /locus-tag="y0369" /function="putative regulator" /note="residues 26 to 400 of 401 are 84.79 pct identical to residues 1 to 375 of 376 from E. coli K12 : B3791" /codon-start=1 /transl-table=11 /product="putative regulator" /protein-id="AAM83958.1" /db-xref="GI:21957054" /translation="MLLYVSIFVVPPLRVPRIG YAGDEMIPFNTPPIVGTIELGYMQA AMSSGKLCGGGFTTRCQQWMEKRFNCPKVLLTP SCTASLEMAALLLDIKPGDEVIMP SFTFVSTANAFVLRGAKMVFVDIRPDTMNI DETK IEAAITDKTRVIVPVHYAGVACEM DTIMALAKKHNLVVEDAAQGVMSYKKGALGTI GHIGCSFHETKNYTAGGEGGATL INDP SLIDRAEIIREKGTNRSQFFRGQVDKYTWR DIGSSYLMSDLQAAYLWGOLEAAE QINERRLALWHGYNAFKPLADAGRIDLFPVPGN VVQNAHMFYIKLRDIEERSAFISY LKEADIMAVFHYIPLHACPAGEAFGRMAGEDRFT SKESERLVRLPIFYNLTDVNQSTV INTVLSEFFV" /gene="wzxE" /locus-tag="y0370" /gene="wzxE" /locus-tag="y0370" /function="putative carrier" /note="residues 1 to 416 of 418 are 75.00 pct identical to residues 1 to 416 of 416 from E. coli K12 : B3792; residues 1 to 416 of 418 are 75.00 pct identical to residues 1 to 416 of 416 from GenPept : >emb CAD09390.1  (AL627279) putative lipopolysaccharide biosynthesis
gene	412207..413412	
CDS	412207..413412	
gene	413414..414670	
CDS	413414..414670	

		protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="putative cytochrome" /protein-id="AAM83959.1" /db-xref="GI:21957055" /translation="MSLAKASIWACSTLIKIGV GLLVVKLLAVTFGPGSGVGQAGNFR QLIIVLGVLSGAGIFNGITKYVAEYHQPERLRA MLGTSSTIVLGFSTLLALVFLAA KPVSIALFGHADYQNVVRAIAFIQMGIAYNLFL AILKGYRDAMGNALAIIGGSLIGV VAYYICFQIGGYSGALVGLGLVPALVVLPAAML YRRRTIPLRYLKPHWDKALASHLG KFTLMALITSVTLPVAYVMMRHLLANNYGDVAVG IWQGVSSISDAYLQFITASFTVYL LPTLSRLKDKGAISREIFRSLKFLVPAVAASLT VWLLRDFAIWLLFSHQFTAMRDLF AWQLVGDVLKVGSYVFGYLVIAKASLRFYILAEV SQFLLLTGFAYWLIPMNGSLGAAQ AYMATYIVYFALCSCAFLVYRRHSAP" /gene="wecF" /locus-tag="y0371" /gene="wecF" /locus-tag="y0371" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); similar to B3793 in E. coli K-12; residues 1 to 359 of 361 are 64.90 pct identical to residues 1 to 357 of 359 from GenPept : >emb CAD09389.1  (AL627279) conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="TDP-Fuc4NAc:lipid II Fuc4NAc transferase" /protein-id="AAM83960.1" /db-xref="GI:21957056" /translation="MITLTHVLGSDIPHHNLTVL RFFNDVLAKCLPVEQVRHFMVAAK ETAPFSSFPQLDINTYSDKKALAEAVIARAQADR SARFFWHGQFNVTLWLALLSGKIK PGQVYVHWVGADLYEDAKSLKFRFLFYLLRRIAQG RVGHVFATRGDLIHYQQRHPRVFA SLLYFPTRMDPALTAINIDKFLAGPMTILVNGSG DTNRRHIEALKAIHQFGPDVRVI IPMGYPANNEAYIEQVRQAGLALFSQDNLRILTE QIPFDYLLNILRECDLGYFIFNRQ QGIGTLCLLTQFGVFFVLSRKNPFWDLAEQHIP VFFYGDITLDEPMIREAQRLAGLD KQAI AFNPNIYEGWKQALALAEHP" /gene="wecF" /locus-tag="y0372" /gene="wecF"
gene	414693..415778	
CDS	414693..415778	
gene	415775..417139	
CDS	415775..417139	

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/locus-tag="y0372"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 444 of 454
are 77.97 pct identical to
residues 1 to 445 of 450 from E.
coli K12 : B3793; residues 1 to
444 of 454 are 77.97 pct identical
to residues 1 to 445 of 450 from
GenPept :
>gb|AAG58989.1|AE005610-13
(AE005610) TDP-Fuc4NAc:lipidII
transferase; synthesis of
enterobacterial common antigen
(ECA) [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="TDP-Fuc4NAc:lipidII
transferase"
/protein-id="AAM83961.1"
/db-xref="GI:21957057"
/translation="MTLGQFGGLFCIYLIVIFI
LTLTYQEFRRVKFNFNVLFSMLYL
LTFYFGFPLTCLMLVFQFGVAVVPEYLLYAMLSA
TAFYGIYYVTYKTRLRQPRSQPRT
PIFTMNRVETNLTWLLVALVAVGTGVIFFMQNGF
LLFKLDSYSKIFSSDVSGVALKRF
FYFFIPAMLVVYFLKQDRRAWFFFLASTVAFGIL
TYVIVGGTRANIIAFLSLFIFIGI
VRGWITLWMLAAGVFGIVGMFWLALKRYGLDVN
GAFAFYTFLYLTRDIFSPWENLGL
LLQNYDKIDFQGLAPIVRDFYVFIPSAWPERPD
LVLNTANYFTWDVLNDHSGLSAISP
TLIGSLVVMGGVFIPLGAIVVGLIHKWFDWLYE
QGKAESNRYKAAILQSF CFGAVFN
IIVLAREGLDSFVSRVVFVCFIFGACLVAKLLY
WLFDTAGLIKRGIKSNRLSTPNA GNQL"
/gene="wecG"
/locus-tag="y0373"
/gene="wecG"
/locus-tag="y0373"
/function="enzyme; central
intermediary metabolism:
Sugar-nucleotide biosynthesis,
conversions"
/note="synthesis of
enterobacterial common antigen
(ECA); residues 1 to 246 of 246
are 70.73 pct identical to
residues 1 to 246 of 246 from E.
coli K12 : B3794"
/codon-start=1
/transl-table=11
/product="probable
UDP-N-acetyl-D-mannosaminuronic
acid transferase"
/protein-id="AAM83962.1"

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gene 417148..417888

CDS 417148..417888

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NAEKLKAEDDTALCELIKNAEYLYADGISMVRA
IRRKYPQAELSRVAGADLWEALMQ
RAGQQGTPVFLVGGKPDVLAETAKLRAQWNVNL
VGSQDGYFTPEQREALFARIAASG
AAIVTVAMGSPKQEIFMRDCRKFYPDALYMGVGG
TYDVFTSHVKRAPKIWNMGLEWL
YRLLAQPSRIRRLKLLKFVGYYSGRLL"
gene      complement(418178..4182 /locus-tag="y0374"
61)
CDS        complement(418178..4182 /locus-tag="y0374"
61)

/codon-start=1
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/product="hypothetical"
/protein-id="AAM83963.1"
/db-xref="GI:21957060"
/translation="MNEGLTAPRGTPVAYAITTP
TARFPFN"
gene      418412..419803
CDS        418412..419803
/locus-tag="y0375"
/locus-tag="y0375"
/function="putative transport"
/notes="residues 1 to 454 of 463
are 79.73 pct identical to
residues 1 to 452 of 461 from E.
coli K12 : B3795; residues 1 to
454 of 463 are 80.39 pct identical
to residues 1 to 452 of 461 from
GenPept :
>gb|AAG58991.1|AE005611-1
(AE005611) putative amino
acid/amine transport protein
[Escherichia coli O157:H7 EDL933]"
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acid/amine symporter"
/protein-id="AAM83964.1"
/db-xref="GI:21957061"
/translation="MADNAEKKGLHRGLEARHIE
LIALGGTIGVGLFMGSASTLKWAG
PSVLLAYIIAGLFVFFIMRAMGEMLYLEPVAGSF
AVYAHKYLSPYFGYLTANGYWFWM
IavgISEITAIGVYVQFWFPEIPQWLPAIAGVAI
VALANLAAVKLYGELEFWFAMIKV
TTIIVMILVGLGVIFFGFGNHGQPIGFDNLTAHG
GFFAGGWKGFLFALCIVVASVQGV
ELVGITAGEARNPQVTLRRAINNILWRILIFYVG
AIFVIVITFPWNGIGTEGSPFVLT
FAKIGIVAAAGIINFVILTAALSGCNSGMYSGGR
MLYALAKNRQLPAGLTKLSASGVP
VYCIIATITLCLLVGSSSLNYIIPNPQQVFVYVYSA
SVLPGMVPWFVVLVCQLRFRQVHK
AALQQHPFKSILFPYVNYLTI AFLICVLVGMGIN
PDTRL SLLVGAIFLALVTGCVFVL
GMHKKPAMEAERL"
/locus-tag="yt006"
/locus-tag="yt006"
/product="tRNA-Arg"
/notes="anticodon: CCG"

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tRNA	420112..420184	/locus-tag="yt007"
		/product="tRNA-His"
		/note="anticodon: GTG"
gene	420204..420287	/locus-tag="yt008"
tRNA	420204..420287	/locus-tag="yt008"
		/product="tRNA-Leu"
		/note="anticodon: CAG"
gene	complement(420253..420741)	/locus-tag="y0376"
CDS	complement(420253..420741)	/locus-tag="y0376"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83965.1"
		/db-xref="GI:21957062"
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gene	420366..420439	/locus-tag="yt009"
tRNA	420366..420439	/locus-tag="yt009"
		/product="tRNA-Pro"
		/note="anticodon: TGG"
repeat-region	421164..421873	/note="insertion element"
		/insertion-seq="IS1541a"
gene	421258..421767	/locus-tag="y0377"
CDS	421258..421767	/locus-tag="y0377"
		/function="IS and transposon related functions"
		/note="IS1541a; residues 1 to 169 of 169 are 100.00 pct identical to residues 1 to 169 of 169 from GenPept : >gb AAC82673.1  (AF074611) transposase [Yersinia pestis]"
		/codon-start=1
		/transl-table=11
		/product="putative transposase"
		/protein-id="AAM83966.1"
		/db-xref="GI:21957063"
		/translation="MRSGNCKCSTRNQKGVPMRD EKSLAHTRWNCKYHIVFAPKYRRQ VFYREKRAAIGSILRKLCEKWNVILEAEYCVDH IHMLLEIPPMSVSGFMGYLKGS SLMLYEQGDLKFKYRNREFWRCGYVYDVTGKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK"
gene	complement(421960..423180)	/gene="hemY"
		/locus-tag="y0378"
CDS	complement(421960..423180)	/gene="hemY"
		/locus-tag="y0378"
		/function="enzyme; biosynthesis of cofactors, carriers: Heme, porphyrin"
		/note="a late step of protoheme IX synthesis; residues 1 to 395 of

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406 are 70.63 pct identical to
residues 1 to 395 of 398 from E.
coli K12 : B3802"
/codon-start=1
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/product="hemY protein"
/protein-id="AAM83967.1"
/db-xref="GI:21957064"
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AIMLVLLLVAFFIVEVWLRIRFTGARTGWFLG
RKRRTRARNQMKAALIKLAEGDFLO
VEKLLTRNADHAEQPMVNYLLAAEAQQRGDEF
R
TNQYLERAAEVAADGDQLPVNITRV
RIQLAQGHIHAARHGVDRLDQAPRHPEVLRLE
QAYLRSGAYRSLDILPAMSKTQI
HIPEEVAALEQQAYIGIMNQMADEGSEGLKRW
KDQSRKVRNEIPLQVALAEHLIEC
DDHDVQAKIILDLSKHQYDERLALLIPRLKAGN
P
EPLEKSLRQQIKQHGAATPLLNSTL
GQLMLKHGEWEKASEAFKAALQRPDGYDYAWLA
DALDKLHRPEDAAQARREGLLLTL
RQNGESSALTCLIH"
gene      complement(423183..4243 /gene="hemX"
16)
CDS      complement(423183..4243 /locus-tag="y0379"
16)      /gene="hemX"
          /locus-tag="y0379"
          /function="enzyme; biosynthesis of
          cofactors, carriers: Heme,
          porphyrin"
<-----User Break----->
145 of 145 are 46.15 pct identical
to residues 1 to 126 of 127 from
GenPept : >gb|AAL22425.1|
(AE008864) putative
acetyltransferase [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM84010.1"
/db-xref="GI:21957111"
/translation="MNLGAISTLLWLLAMKLTI
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AWQQWITEGRPLFAARFNRLLGAVKVAVYDQQA
ELQDLCVREVTRRRGVGLYLIET
LRQLPEIKHWYINGGDLTAAERFQMNSFMLACGF
SHEAQGWRR"
gene      470375..471505 /gene="livK"
CDS      470375..471505 /locus-tag="y0422"
          /gene="livK"
          /locus-tag="y0422"
          /function="transport; transport of
          small molecules; amino acids,
          amines"
          /note="residues 12 to 376 of 376
          are 75.34 pct identical to
          residues 6 to 369 of 369 from E.
          coli K12 : B3458; residues 12 to
          376 of 376 are 75.61 pct identical

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to residues 6 to 369 of 369 from  
 GenPept :  
 >gb|AAG58565.1|AE005569-5  
 (AE005569) high-affinity  
 leucine-specific transport system;  
 periplasmic binding protein  
 [Escherichia coli O157:H7 EDL933]"  
 /codon-start=1  
 /transl-table=11  
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 leucine-specific leucine-specific-b  
 inding periplasmic protein of  
 high-affinity branched-chain amino  
 acid ABC transporter transport  
 system; periplasmic binding  
 protein"  
 /protein-id="AAM84011.1"  
 /db-xref="GI:21957112"  
 /translation="MGNSRMKLTGKGVLLAGCMA  
 MAMSHSVLAQDIKVAIVGAMSGPV  
 AQYQDMQFTGARQAIADINASGGIKGDKLVGVEY  
 DDACDPKQAVAVANKVINDGIRYV  
 IGHLCSSSTQPASDIYEDEGVIMITPAATNADLT  
 TRGYKIMIRTTGLDSQDGQTAAYK  
 IVETIKPKRIAVVHDKQQYGEGLARSVRDSLKEQ  
 GAEVVLFEQVTAGDKDFSTLVARL  
 KKENVDFVYFGGYFPEMGQILRQAKQAGLTARFM  
 GPEGVGNSSLSNIAGEASEGMLVT  
 LPKRYDQVPANQPIVDALKAKKLDPTGPFVWTTY  
 AALQSLTTAMERTGSKEPADLAND  
 LKTGKPVETVMGPLSWDDKGD LKGF EFGIF EFWHA  
 DGSSTAVK"  
 /gene="livH"  
 /locus-tag="y0423"  
 /gene="livH"  
 /locus-tag="y0423"  
 /function="transport; transport of  
 small molecules; amino acids,  
 amines"  
 /note="residues 1 to 308 of 308  
 are 87.33 pct identical to  
 residues 1 to 308 of 308 from E.  
 coli K12 : B3457; residues 1 to  
 308 of 308 are 87.66 pct identical  
 to residues 1 to 308 of 308 from  
 GenPept : >gb|AAL22423.1|  
 (AE008864) ABC superfamily  
 (membrane), branched-chain amino  
 acid transporter, high-affinity  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="high-affinity  
 branched-chain amino acid ABC  
 transport system membrane  
 permease"  
 /protein-id="AAM84012.1"  
 /db-xref="GI:21957114"  
 /translation="MSEQFLYFLQQMFNGITLGS  
 TYALIAIGYTMVYGIIGMINFAHG  
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 VSIIVASTYGSIERVAYKPVRRS

gene	471686..472612
CDS	471686..472612

gene	472609..473895	<p>KRLIALISAIGMSIFLQNYVSLTQGSRDALPSL VTGQWTLGESNGFAATISTMQLTI WIVTFLAMLALTLFIRYSRMGRACACAECLKMA SLLGINTDRVISLTFVIGALMAAV AGVLLGQFYGVINPYIGFMAGMKAFTAAVLGGIG SIPGAMIGLVLGVAEALTSAYLS TEYKDAVSFALLIVVLLVMPGTILGRPEVEKV" /gene="livM" /locus-tag="y0424" /gene="livM" /locus-tag="y0424" /function="transport; transport of small molecules; amino acids, amines" /note="residues 1 to 428 of 428 are 79.43 pct identical to residues 1 to 425 of 425 from E. coli K12 : B3456" /codon-start=1 /transl-table=11 /product="inner membrane permease of high-affinity branched-chain amino acid ABC transport system" /protein-id="AAM84013.1" /db-xref="GI:21957115" /translation="MKQLNEFVNAISSFVLLVLA SFVMGLQLQDGTRLVVQGASEVR WLWIGAGCLVVFCFQLVRLPIQQGIIKKVSGPAWV LPSFDGTTPRQKLLAAVVVIAAVA WPFLVSRGSVDIATLTLIYVMLGLGLNVVVGLSG LLVLGYGGFYAIGAYTYALLNHYY GLGFWESLPLAGITAALSGFLGFVPLRLRGDYL AIVTLGFGEIVRILLNNTEITGG PNGISQIPKPTILGLEFSRTAKDGGWDTFHNFEG LTYDPSHRIIFLYLVALLLVILT FVINRLRLMPLGRAWEALREDEIACRSLSGLSPTK IKLTAFTISAAGFAGFAGTLFAARQ GFVSPESFTFVESAFVLAIVVLGGMGQSQAFILA AVLLVVSRELMRDNLNAYSMLLLGA LMVLMMIWRPQGLLPMKRPQLKLKVADVKAKQGE QA"</p>
CDS	472609..473895	
gene	473892..474659	<p>/gene="livG" /locus-tag="y0425" /gene="livG" /locus-tag="y0425" /function="transport; transport of small molecules; amino acids, amines" /note="residues 4 to 255 of 255 are 82.14 pct identical to residues 3 to 254 of 255 from E. coli K12 : B3455; residues 4 to 255 of 255 are 83.33 pct identical to residues 3 to 254 of 255 from GenPept : &gt;gb AAL22421.1  (AE008864) ABC superfamily (atp-bind), branched-chain amino acid transporter, high-affinity [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="ATP-binding component of</p>
CDS	473892..474659	



		high-affinity branched-chain amino acid ABC transport system"
		/protein-id="AAM84014.1"
		/db-xref="GI:21957116"
		/translation="MNGQPLLTV EGLSMRFGGLL AVNNVGLTLNQGEIVSLIGPNGAG KTTIFNCLTGFYRPTGGTIKLRERHLEGLPGQMI ARMGVIRTFQHVRLFREMTVIE NL LVAQHQLKSGIFAGLLKTPGFRRAEADALARA TWLERVGLLALANRQAGNLAYGQQ RRLEIARCMVTRPELLMLDEPAAGLNPKETDELN QLIMELRDQHQVSVLLIEHDMKLV MGISDRIYVVGQTPLAQGLPAEIRNNPDVIRAY LGE"
gene	474674..475405	/gene="livF"
		/locus-tag="y0426"
CDS	474674..475405	/gene="livF"
		/locus-tag="y0426"
		/function="transport; transport of small molecules; amino acids, amines"
		/note="residues 11 to 243 of 243 are 87.12 pct identical to residues 9 to 241 of 241 from E. coli K12 : B3454"
		/codon-start=1
		/transl-table=11
		/product="ATP-binding component of leucine transport"
		/protein-id="AAM84015.1"
		/db-xref="GI:21957117"
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gene	475633..476094	/locus-tag="y0427"
CDS	475633..476094	/locus-tag="y0427"
		/note="residues 26 to 113 of 153 are 28.40 pct identical to residues 181 to 264 of 413 from GenPept : >gb AAC44570.1  (U61140) ORF1 [Mycoplasma mycoides subsp. mycoides SC]"
		/codon-start=1
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		/db-xref="GI:21957118"
		/translation="MMDGISNKMQLQGLSAVRSF AFLTADMLNLITKNKGDNHEYKVT SSHVNNDKLQGPKGILKATKNHAELKNETIASGE KKTISFDKLVHREIPDREQASYID NLSLNRNIYLDTSADRECRIPQVLSPPQNVDSG TKKPFWISKYLCITTLTY"
gene	complement(476209..477315)	/locus-tag="y0428"
CDS	complement(476209..477315)	/locus-tag="y0428"

15)

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/note="residues 16 to 44 of 368
are 51.61 pct identical to
residues 242 to 272 of 621 from
GenPept : >gb|AAF48396.1|
(AE003497) CG9521 gene product
[Drosophila melanogaster]"
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DGSADFSIRPGDIQNMSLNGIPVQEIDYNLQEAR
FVSTHAFSNQSYHVSFNITANALK
HIRMGATIGGVLHSEGVSYSVRSPQGVAFNQSGN
QCEFFDPTEIAPSHALYIEPKFR
LGSAIWQLKSLDLHLLDSTADNHGLHAPLVNGP
ANRFCIHYPAGITQNRMYMISASN
LNLGAESSRYFQKDNQGEHIINYKVTLNHEDS
EADFSLPKEKKFIQLKSDTSSGGE
AQMCSPIRVYSTDTTDKGHYDTLNFITPLA
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gene complement(477393..4779 /locus-tag="y0429"

11)  
CDS complement(477393..4779 /locus-tag="y0429"

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11)
/note="residues 61 to 118 of 172
are 29.31 pct identical to
residues 781 to 838 of 987 from
GenPept : >dbj|BAB75624.1|
(AP003594) ORF-ID:alr3925
hypothetical protein [Nostoc sp.
PCC 7120]"
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GYQISIKNPLILTRQSDAFSAIEQ
TFSPAIEVRWGNRNLRLLLSAVPESESFPVPQATR
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HGQLTLVFEVNS"
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gene complement(477973..4786 /locus-tag="y0430"

35)  
CDS complement(477973..4786 /locus-tag="y0430"

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35)
/note="residues 6 to 174 of 220
are 27.27 pct identical to
residues 1 to 173 of 238 from
GenPept : >emb|CAA87760.1|
(Z47800) CotB [Escherichia coli]"
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QQPLLATPLKLTGLPGROSGKIFL
HALGAPEQEQQVYRLAVVPSNHLKISGNNTAVVGV
QISYMLIRHLPASIQHQTWRICI
AGKPELHNTGNTRLYWHQLQAQGMIDDFTLYPG
RYRQLAFNELQGVVEDQAVNLQCP SG"
gene      complement(478592..4793
11)
CDS       complement(478592..4793 /locus-tag="y0431"
11)

/Note="residues 11 to 221 of 239
are 21.02 pct identical to
residues 3 to 206 of 236 from
GenPept : >emb|CAD08770.1|
(AL627266) putative fimbrial
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84020.1"
/db-xref="GI:21957122"
/translation="MPRRLLIPIGTFMKYLYSILS
IALLLAPGSATHGQLLATPRTIAV
EAQELKRTVQVYNSGDTPLYLDITLQRVDNPGVN
PERKTPISEISQEMIFNPNRITL
GPRQKRDITLIPLKSPVQETLYRLYINPVLNIKA
VGDGEDKSKVHAPMTISIGYGVLI
HHLPPAAQAQTRHWQHQCSTTGELTLTATGTVHKS
FKQLESGGNAALADSLNLYPGTAL
TLPVKQLNGEVDGEKFSLRCH"
gene      complement(479296..4816
44)
CDS       complement(479296..4816 /locus-tag="y0432"
44)

/Note="residues 53 to 775 of 782
are 20.33 pct identical to
residues 49 to 830 of 869 from
GenPept : >gb|AAC41416.1| (M55661)
colonization factor antigen c
[Escherichia coli]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84021.1"
/db-xref="GI:21957123"
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AAEENNSLQLLGVLDKTLPSPTTFSEEEQLQF
NQQNYRHHNNISEESILLGEILSQ
IPYLQCKTGCDYTLSGHRVALDKVNNNTLITNHN
NRYLMPTTITWGLVSNQSLDLRMTA
AHYRAMSVRGQSYIGLPWQSYGFASWFYNAIQSQ
NTLQSQNTMPSQSTYQPVNRPQYQ
RLTKQIGISWYILQKNFSALYLRTRQNNDLNNAG
SVHTLINPALDQFVTLGSQSYLAI
DKPSTGISVLYAAQDGDYIEYRDNLIRRIPAQL
GRNEIDYSQLPGGYYNVEIRLVDR
LGRIVSQENQTSISIGNQTNNGWFLTMGKGFPAKG

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KKTPLRVQFGRSRVIESVQTNITL  
 LKDDAHHWAVEANVSRLSLNKNITPTGGLMSG  
 EKRSGGYVRLNGGNNTLGYFSLAR  
 YQSPYVSRYAPDSGSTSGSYTRRIGPTQLSYQFN  
 QYRNNRQHRIQSGWDWQLPQFNLA  
 LSLGLQNGGQWNSHNNYGVFLNTTSLFGQSNASI  
 NTAYTQQQLNTSASYQKEFIDNYG  
 ASTLGVSGSASGKLNSVGGFAKRSRSGRDISGRV  
 GIDNQITNGGISYNGMLALSSQGV  
 ALGRSSYSGAALLIKAPALGGTPYSFHVESPIIT  
 GGGTYAIPVPRYQDRFFVRTHITDR  
 SDMDMNIQLPVNIVRAHPGQVFSGEADITLNLly  
 SGFLKNAQGLPVSGVIEETGDTAY  
 PNGLESINAQNRLQAITVHGPGSGRYRCMDMSQPT  
 HIYLCHAD"

gene complement(481896..4823 /locus-tag="y0433"  
 87)  
 CDS complement(481896..4823 /locus-tag="y0433"  
 87)

/note="residues 3 to 157 of 163  
 are 26.06 pct identical to  
 residues 4 to 164 of 170 from  
 GenPept : >gb|AAC41415.1| (M55661)  
 colonization factor antigen b  
 [Escherichia coli]"  
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 /transl-table=11  
 /product="hypothetical"  
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 /db-xref="GI:21957125"  
 /translation="MMKKTVIAIITMATLTSTAA  
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 LGDKLVSLAAPVILSEFNNKKEF  
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 VSAKEPNNAVGGKEYSGVIQLRLE PSA"

gene 482942..484261  
 CDS 482942..484261

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 /gene="ugpB"  
 /locus-tag="y0434"  
 /function="transport; transport of  
 small molecules; carbohydrates,  
 organic acids, alcohols"  
 /note="sn-glycerol 3-phosphate ABC  
 transport system; residues 6 to  
 439 of 439 are 80.18 pct identical  
 to residues 4 to 437 of 438 from  
 E. coli K12 : B3453; residues 5 to  
 439 of 439 are 82.06 pct identical  
 to residues 3 to 437 of 438 from  
 GenPept : >gb|AAL22417.1|  
 (AE008864) ABC superfamily  
 (peri-perm), sn-glycerol  
 3-phosphate transport protein  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="periplasmic binding  
 protein"  
 /protein-id="AAM84023.1"  
 /db-xref="GI:21957126"  
 /translation="MFNNSIHKVSICIALTLTFS

ANAMAVTEIPFWSMEGELGKEVD  
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 RSGKAPAILQVYEVGTATMMASKA  
 IKPVYQVFKDANIDFDESVEVPTVAGYYTDSKTG  
 RLLSQPFNSSTPVLYYNKEAFKKA  
 GLDPEQPPKTWQELAADTKLRAAGSSSCGYASGW  
 QGWIQIENFSAWHGQPIASRNNGF  
 DGTDAVLEFNKPLQVKHIQLLSDMNKKGDFTYFG  
 RKDESTSKFYNGDCAITTASSGSL  
 ASIRHYAKFNFGVGMMPYDADAKNAPQNAIIGGA  
 SLWVMDGKDKETYKGVAEFLQYL  
 KPEIAAEWHQKTGYLPITTAAYELTKQQGFYEQN  
 PGADVATRQMLNKPPLPYTKGLRL  
 GNMPPQIRTVVDEELEAVNTAKKTPQAALDNSVKR  
 GDVLLRRFEQANK"

gene 484559..485446

CDS 484559..485446

/gene="ugpA"  
 /locus-tag="y0435"  
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 /locus-tag="y0435"  
 /function="transport; transport of  
 small molecules; carbohydrates,  
 organic acids, alcohols"  
 /note="sn-glycerol 3-phosphate ABC  
 transport system; residues 1 to  
 295 of 295 are 79.32 pct identical  
 to residues 1 to 295 of 295 from  
 E. coli K12 : B3452; residues 1 to  
 295 of 295 are 80.33 pct identical  
 to residues 1 to 295 of 295 from  
 GenPept : >gb|AAL22416.1|  
 (AE008864) ABC superfamily  
 (membrane), sn-glycerol  
 3-phosphate transport protein  
 [Salmonella typhimurium LT2]"  
 /codon-start=1  
 /transl-table=11  
 /product="integral membrane  
 protein, permease"  
 /protein-id="AAM84024.1"  
 /db-xref="GI:21957127"  
 /translation="MSPSRPGFSCSWLPYLLVLP  
 QLAITAIFLWPAGEALWYSVQTL  
 DPFGLSSEFVGLSNFIQLFQDEYYLASFYTTLIF  
 SALVAGIGLIVSLFLAAMVNYVLR  
 GSRLYQTLLILPYAVAPAAVLWIFLDPGLGL  
 ITHALAKLGYSWNHAQNSGQAMFL  
 VVLASVWKQISYNLFFLAALQSIPKSLVEAAAI  
 DGAGPVRRFFNLVLPILISPVSFLL  
 LVVNLVYAFFDTFFPVIDAATGGPGPVQATTLLIYK  
 IYREGFAGLDLSSSAAQSVILMLL  
 VIGLTVIQFRFVERKVRVQ"

gene 485443..486288

CDS 485443..486288

/gene="ugpE"  
 /locus-tag="y0436"  
 /gene="ugpE"  
 /locus-tag="y0436"  
 /function="transport; transport of  
 small molecules; carbohydrates,  
 organic acids, alcohols"  
 /note="sn-glycerol 3-phosphate ABC  
 transport system; residues 1 to  
 281 of 281 are 77.58 pct identical  
 to residues 1 to 281 of 281 from

E. coli K12 : B3451; residues 1 to 281 of 281 are 79.71 pct identical to residues 1 to 281 of 281 from GenPept : >gb|AAL22415.1| (AE008864) ABC superfamily (membrane), sn-glycerol 3-phosphate transport protein [Salmonella typhimurium LT2]"  
/codon-start=1  
/transl-table=11  
/product="inner membrane permease"  
/protein-id="AAM84025.1"  
/db-xref="GI:21957128"  
/translation="MIENRRGLDIFCHIMLIIGV  
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PMTLIPGPHLWQNIISHIWHAGVGNNSPPFGLMLL  
NSFVMAFAITVGKIIVSILSAYAI  
VYFRFPLRNLFWLIFLTLMLPVEVRIFPTIEVI  
ANLNLDDSYTGLTLPLMASATATF  
LFRQFFMTLPDELLEAARIDGAGAMRFFWDIVLP  
LSKTNLAALFVITFIYGNQYLPW  
ILITSASMGTAAGIRSMISTSGAPTOWNQVMA  
AMILTIPPVVVLLMQRWVFRGL VDSEK"  
/gene="ugpC"  
/locus-tag="y0437"  
/gene="ugpC"  
/locus-tag="y0437"  
/function="transport; transport of small molecules; carbohydrates, organic acids, alcohols"  
/note="sn-glycerol 3-phosphate ABC transport system; residues 1 to 355 of 357 are 75.56 pct identical to residues 14 to 369 of 369 from E. coli K12 : B3450; residues 1 to 355 of 357 are 75.56 pct identical to residues 14 to 369 of 369 from GenPept :  
>gb|AAG58556.1|AE005568-6 (AE005568) ATP-binding component of sn-glycerol 3-phosphate transport system [Escherichia coli O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
/product="ATP-binding component"  
/protein-id="AAM84026.1"  
/db-xref="GI:21957129"  
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KQIDLVDADGEFIVMVGPSGCGKS  
TLRLMVAGLERITTTGDIYIGDQRTDLEPKDRGI  
AMVFQNYVLYPHMNVFDNMAYGLK  
IRFGQEQIRQVRDEAARILELQPLLKRKPRELS  
GGQRQVRAMGRAIVREPAVFLFDE  
PLSNLDALRVQMILLELQQLHRLRKTTSLYVTHD  
QVEAMTLAQRVIVMNGVVAEIGT  
PSEVYKRPAFLFVASFVIGSPAMNLLDGTVPDGR  
TFILSDGLTLPLLEIPQWPQWGGRRLL  
TLGIRPEHIQQTSAQGVPMNLLTLELLGADNLA  
HGLWGGQSIARLSHEEMPVAGST  
LHLYLPPAALHFFDTSGLRIEP"  
/gene="ugpQ"

gene 486295..487368

CDS 486295..487368

gene 487365..488114

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CDS          487365..488114          /locus-tag="y0438"
                                         /gene="ugpQ"
                                         /locus-tag="y0438"
                                         /function="enzyme; central
                                         intermediary metabolism: Pool,
                                         multipurpose conversions"
                                         /note="residues 4 to 247 of 249
                                         are 72.95 pct identical to
                                         residues 3 to 245 of 247 from E.
                                         coli K12 : B3449; residues 4 to
                                         247 of 249 are 73.77 pct identical
                                         to residues 3 to 245 of 247 from
                                         GenPept :
                                         >gb|AAG58555.1|AE005568-5
                                         (AE005568) glycerophosphodiester
                                         phosphodiesterase, cytosolic
                                         [Escherichia coli O157:H7 EDL933]"
                                         /codon-start=1
                                         /transl-table=11
                                         /product="cytosolic
                                         glycerophosphodiester
                                         phosphodiesterase"
                                         /protein-id="AAM84027.1"
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                                         QLDAGDWFSKAFRGERLPLLSEVA
                                         ARCAQHGMGAANIEIKPTTGTDAPTGRAIALAARA
                                         LWQGPPIPLLSSFSVDALAAQQL
                                         AVPELPRGLLLLDKWDDNWAALTQLDCVSLHINH
                                         KQLTAERVALLKAAGLRILVYTVN
                                         QPERARELLNWGVDCICTDRIDLLGSDFTCG"

gene          488215
<-----User Break----->

=> d hist

(FILE 'HOME' ENTERED AT 04:02:48 ON 01 OCT 2008)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 04:03:14 ON 01 OCT 2008
SEA BIOFILM AND REMOV?(P)BIOFILM AND PROTEASE AND ESTERASE AND
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0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
0* FILE ESBIOBASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
1 FILE GENBANK
1 FILE IFIPAT

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0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
11 FILE USPATFULL
4 FILE USPAT2
0* FILE WATER
L1 QUE BIOFILM AND REMOV?(P) BIOFILM AND PROTEASE AND ESTERASE AND
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FILE 'GENBANK, IFIPAT, USPATFULL, USPAT2' ENTERED AT 04:05:30 ON 01 OCT 2008

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L2      17 S L1
L3      13 DUP REM L2 (4 DUPLICATES REMOVED)

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=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
45.35	48.16

FULL ESTIMATED COST

STN INTERNATIONAL LOGOFF AT 04:07:12 ON 01 OCT 2008